

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 13:16:25 ; Search time 22 Seconds
(without alignments)
635.938 Million cell updates/sec

Title: US-10-069-385-1

Perfect score: 1491
Sequence: 1 VAEYTPWRDAETGERLVC.....RVAMPGLERSVVERLPVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/2/iaa/5A COMB.pcp.*
- 2: /cgn2_6/ptodata/2/iaa/5B COMB.pcp.*
- 3: /cgn2_6/ptodata/2/iaa/6A COMB.pcp.*
- 4: /cgn2_6/ptodata/2/iaa/6B COMB.pcp.*
- 5: /cgn2_6/ptodata/2/iaa/PCTUS COMB.pcp.*
- 6: /cgn2_6/ptodata/2/iaa/backfiles1.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1491	100.0	300	2	US-08-794-796-2
2	1491	100.0	300	4	US-09-632-277A-2
3	1491	100.0	300	4	US-09-523-323-52
4	1476.5	99.0	299	3	US-09-286-529-17
5	1034	69.3	211	3	US-09-286-529-20
6	855	57.3	146	4	US-09-523-323-59
7	841	56.4	153	3	US-09-286-529-2
8	440.5	29.5	401	3	US-08-974-022-6
9	440.5	29.5	401	3	US-09-042-785A-12
10	440.5	29.5	401	3	US-08-795-445A-6
11	440.5	29.5	401	3	US-08-795-447A-6
12	440.5	29.5	401	3	US-08-974-186-6
13	440.5	29.5	401	3	US-08-795-446B-6
14	440.5	29.5	401	3	US-09-153-927-1
15	440.5	29.5	401	4	US-09-072-993C-1
16	440.5	29.5	401	4	US-08-706-945D-128
17	440.5	29.5	401	4	US-10-039-785-5
18	440.5	29.5	401	4	US-08-577-788C-6
19	440.5	29.5	401	4	US-08-577-788C-56
20	433	29.0	161	4	US-09-632-277A-3
21	425.5	28.5	401	3	US-08-974-022-2
22	425.5	28.5	401	3	US-08-795-445A-2
23	425.5	28.5	401	3	US-08-795-447A-2
24	425.5	28.5	401	3	US-08-974-186-2
25	425.5	28.5	401	3	US-08-795-446B-2
26	425.5	28.5	401	4	US-08-706-945D-124
27	425.5	28.5	401	4	US-08-577-788C-2

Sequence 55, Appl
Sequence 4, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 4, Appl
Sequence 126, App
Sequence 4, Appl
Sequence 54, Appl
Sequence 50, Appl
Sequence 20, Appl
Sequence 20, Appl
Sequence 58, Appl
Sequence 136, App
Sequence 142, App
Sequence 141, App
Sequence 130, App

ALIGNMENTS

RESULT 1

US-08-794-796-2
; Sequence 2, Application US/08794796
; Patent No. 5885800
; GENERAL INFORMATION:
; APPLICANT: Emery, John
; APPLICANT: Tan, KB
; APPLICANT: Truneh, Alem
; APPLICANT: Young, Peter
; TITLE OF INVENTION: Tumor Necrosis Related Receptor,
; TITLE OF INVENTION: TR4
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/794,796
; FILING DATE: 04-FEB-1997
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Han, William T
; REGISTRATION NUMBER: 34,344
; REFERENCE/DOCKET NUMBER: GH50000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5219
; TELEFAX: 610-270-4026
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 300 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: pro-ein
US-08-794-796-2
Query Match 100.0%; Score 1491; DB 2; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.9e-124;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 60
D5 30 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 89
QY 51 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 120
D5 90 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 149
QY 121 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 180
D5 150 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 209
QY 161 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 240
D5 210 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 269
QY 241 GALLVRLLOALRVARMPLGERSVRERFLPVH 271
D5 270 GALLVRLLOALRVARMPLGERSVRERFLPVH 300

RESULT 2
US-09-632-277A-2
; Sequence 2, Application US/09632277A
; Patent No. 6599716
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: NT3 A No. 6599716el Member of the TNF-Receptor Supergene Family
; FILE REFERENCE: 01017/35549A
; CURRENT APPLICATION NUMBER: US/09/632,277A
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: US 60/147,297
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent-In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-632-277A-2

Query Match 100.0%; Score 1491; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.9e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 60
D5 30 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 89
QY 61 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 120
D5 90 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 149
QY 121 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 180
D5 150 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 209
QY 161 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 240
D5 210 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 269
QY 241 GALLVRLLOALRVARMPLGERSVRERFLPVH 271
D5 270 GALLVRLLOALRVARMPLGERSVRERFLPVH 300

RESULT 3
US-09-523-323-52
; Sequence 52, Application US/09523323
; Patent No. 6635743
; GENERAL INFORMATION:

APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven X.
APPLICANT: Ulrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/163,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: Patent-In Ver. 2.0
SEQ ID NO 52
LENGTH: 300
TYPE: PRT
ORGANISM: Homo sapiens
US-09-523-323-52

Query Match 100.0%; Score 1491; DB 4; Length 300;
Best Local Similarity 100.0%; Pred. No. 3.9e-124;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 60
D5 30 VAETPTYPWDAETGERLVCAQCPGTFVQRCRDSPTTCGPPRHHTQFWNYLERCR 89
QY 61 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 120
D5 90 YCNVLGGEREEERARACHATHNACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTSQNTQ 149
QY 121 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 180
D5 150 CQCPPTGTSASSSSSEQCPHNCRTALGALNVPSSSHDITCTCTGFPPLSTRVPGAE 209
QY 161 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 240
D5 210 ECECAVIDFVAFQDISIKRLQLLQALEAPEGMPPTPRAGRAALQKLRRLTELLGAQD 269
QY 241 GALLVRLLOALRVARMPLGERSVRERFLPVH 271
D5 270 GALLVRLLOALRVARMPLGERSVRERFLPVH 300

RESULT 4
US-09-286-529-17
; Sequence 17, Application US/09286529
; Patent No. 6297367
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES

FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 17
TYPE: PRT
LENGTH: 299
ORGANISM: Homo sapien
US-09-286-529-17

Query Match 99.0%; Score 1476.5; DB 3; Length 299;
Best Local Similarity 99.6%; Pred. No. 7.5e-123;
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAEPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCR 60
DB 30 VAEPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRAACRTGTGFAAGFCLHASCPPGAGVIAPGTPSNTQ 120
DB 90 YCNVLCGEREEERACHATHNRAACRTGTGFAAGFCLHASCPPGAGVIAPGTPSNTQ 149
QY 121 CQCPPTGTFSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180
DB 150 CQCPPTGTFSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 208
QY 181 ECERAVIDFAFQDISIKRLORLLOALEAGGNGPTPRAGAALCLKRRRLTELLGAQD 240
DB 209 ECERAVIDFAFQDISIKRLORLLOALEAGGNGPTPRAGAALCLKRRRLTELLGAQD 268
QY 241 GALLVLLQALRVARMPGLSRRERFLPVH 271
DB 269 GALLVLLQALRVARMPGLSRRERFLPVH 299

RESULT 5
US-09-286-529-20
Sequence 20, Application US/09/286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1
CURRENT APPLICATION NUMBER: US/09/286,529
CURRENT FILING DATE: 1999-04-05
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
TYPE: PRT
LENGTH: 211
ORGANISM: Homo sapien
US-09-286-529-20

Query Match 69.3%; Score 1034; DB 3; Length 211;
Best Local Similarity 98.9%; Pred. No. 6.6e-84;
Matches 179; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCR 60
DB 30 VAEPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRAACRTGTGFAAGFCLHASCPPGAGVIAPGTPSNTQ 120
DB 90 YCNVLCGEREEERACHATHNRAACRTGTGFAAGFCLHASCPPGAGVIAPGTPSNTQ 149
QY 121 CQCPPTGTFSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180
DB 150 CQCPPTGTFSSSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 209
QY 181 E 181
DB 210 E 210

RESULT 6

US-09-523-323-59
Sequence 59, Application US/09523323
Patent No. 6635743
GENERAL INFORMATION:
APPLICANT: Ebner, Reinhard
APPLICANT: Yu, Guo-Liang
APPLICANT: Ruben, Steven M.
APPLICANT: Ulrich, Stephen
APPLICANT: Zhai, Yifan
TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
FILE REFERENCE: 1488.065000C
CURRENT APPLICATION NUMBER: US/09/523,323
CURRENT FILING DATE: 2000-03-10
EARLIER APPLICATION NUMBER: 60/168,380
EARLIER FILING DATE: 1999-12-02
EARLIER APPLICATION NUMBER: 60/148,326
EARLIER FILING DATE: 1999-08-11
EARLIER APPLICATION NUMBER: 60/142,657
EARLIER FILING DATE: 1999-07-06
EARLIER APPLICATION NUMBER: 60/137,457
EARLIER FILING DATE: 1999-06-04
EARLIER APPLICATION NUMBER: 60/124,041
EARLIER FILING DATE: 1999-03-11
EARLIER APPLICATION NUMBER: 09/252,656
EARLIER FILING DATE: 1999-02-19
EARLIER APPLICATION NUMBER: 60/075,409
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/027,287
EARLIER FILING DATE: 1998-02-20
EARLIER APPLICATION NUMBER: 09/003,886
EARLIER FILING DATE: 1998-01-07
EARLIER APPLICATION NUMBER: 08/822,953
EARLIER FILING DATE: 1997-03-21
EARLIER APPLICATION NUMBER: 60/013,923
EARLIER FILING DATE: 1996-03-22
EARLIER APPLICATION NUMBER: 60/030,157
EARLIER FILING DATE: 1996-10-31
NUMBER OF SEQ ID NOS: 70
SOFTWARE: PatentIt Ver. 2.0
SEQ ID NO 59
TYPE: PRT
LENGTH: 146
ORGANISM: Homo sapiens
US-09-523-323-59

Query Match 57.3%; Score 855; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 2.8e-68;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 CAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCRYNVLCGEREEERACHAT 79
DB 1 CAQCPGTFVQPCRRDSTTCGCPPRHYTFQWNYLERCRYNVLCGEREEERACHAT 60
QY 80 HNRACRKTGFFAHAGFCLHASCPPGAGVIAPGTPSNTQCPPTGTFSSSSSQ 139
DB 61 HNRACRKTGFFAHAGFCLHASCPPGAGVIAPGTPSNTQCPPTGTFSSSSSQ 120
QY 140 QPHNRCTALGLALNVPGSSSHDTLCT 165
DB 121 QPHNRCTALGLALNVPGSSSHDTLCT 146

RESULT 7

US-09-286-529-2
Sequence 2, Application US/09286529
Patent No. 6297367
GENERAL INFORMATION:
APPLICANT: Catherine Tribouley
TITLE OF INVENTION: NEW MEMBERS OF TNF AND TNFR FAMILIES
FILE REFERENCE: 1408.003/200130.439C1

; CURRENT APPLICATION NUMBER: US/09/286,529
 ; CURRENT FILING DATE: 1999-04-05
 ; NUMBER OF SEQ ID NOS: 25
 ; SOFTWARE: FASTSEQ for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 153
 ; TYPE: PRT
 ; ORGANISM: human
 US-09-286-529-2

Query Match 56.4%; Score 841; DB 3; Length 153;
 Best Local Similarity 100.0%; Pred. No. 5.1e-67;
 Matches 153; Conservative 0; Mismatches C; Indels 0; Gaps 0;
 QY 56 LERCYCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPGTP 115
 DB 1 LERCYCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPGTP 60
 QY 116 SONTQCCPCCPTFFSASSSSSQCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGFFPLSTR 175
 DB 61 SONTQCCPCCPTFFSASSSSSQCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGFFPLSTR 120
 QY 176 VPSABECRAVDFVAFQDISIKRLQRLQALE 208
 DB 121 VPSABECRAVDFVAFQDISIKRLQRLQALE 153

RESULT 2

US-08-974-022-6
 ; Sequence 6, Application US/08974022
 ; Patent No. 6015938
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, William J.
 ; APPLICANT: Lacey, David L.
 ; APPLICANT: Calzone, Frank J.
 ; APPLICANT: Chang, Ming-Shi
 ; TITLE OF INVENTION: OSTEOPROTEGERIN
 ; NUMBER OF SEQUENCES: 53
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Amgen Inc.
 ; STREET: 1840 DeWittland Drive
 ; CITY: Thousand Oaks
 ; STATE: California
 ; COUNTRY: USA
 ; ZIP: 91320-1789
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/974,022
 ; FILING DATE: 12-DEC-1995
 ; CLASSIFICATION:
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/577,788
 ; FILING DATE:
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Winter, Robert B.
 ; REFERENCE/DOCKET NUMBER: A-378
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 401 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-974-022-6

Query Match 29.5%; Score 440.5; DB 3; Length 401;
 Best Local Similarity 41.2%; Pred. No. 4.3e-31;
 Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
 QY 5 PTYPWRDAETGERLVCAQCPCPGTFFVORPCRRDSFTTCGCPPRHYTQFMNLYRCRYCNV 64

DB 26 PKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECLYCSP 85
 QY 65 LCGEREERACHATHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSNTQOQPC 124
 DB 86 VKELQVVKQECNRTHNRVCECKEGRYLETFCLKHSRCPGPGVQVQAGTPERNTVCKRC 145
 QY 125 PGTRFASSSSSQCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGFFPLSTRVPGAEB--C 182
 DB 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTGKNATHDNI---CSGNSESTCKGIDVTLC 202
 QY 183 ERAVIDF 189
 DB 203 ERAFFFF 209

RESULT 9

US-09-042-785A-12
 ; Sequence 12, Application US/09042785A
 ; Patent No. 6194151
 ; GENERAL INFORMATION:
 ; APPLICANT: Busfield, Samantha J
 ; TITLE OF INVENTION: NOVEL MOLECULES OF THE TNF RECEPTOR SUPERFAMILY
 ; TITLE OF INVENTION: AND USES THEREFOR
 ; NUMBER OF SEQUENCES: 31
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: LAHIVE & COCKFIELD, LLP
 ; STREET: 28 State Street
 ; CITY: Boston
 ; STATE: Massachusetts
 ; COUNTRY: USA
 ; ZIP: 02109
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent in Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/042,785A
 ; FILING DATE: 17-MAR-1998
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/938,896
 ; FILING DATE: 26-SEP-1997
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mandragoras, Amy E
 ; REFERENCE/DOCKET NUMBER: MEI-001CE
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (617)227-7400
 ; TELEFAX: (617)742-4214
 ; INFORMATION FOR SEQ ID NO: 12:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 401 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; FRAGMENT TYPE: internal
 US-09-042-785A-12

Query Match 29.5%; Score 440.5; DB 3; Length 401;
 Best Local Similarity 41.2%; Pred. No. 4.3e-31;
 Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
 QY 5 PTYPWRDAETGERLVCAQCPCPGTFFVORPCRRDSFTTCGCPPRHYTQFMNLYRCRYCNV 64
 DB 26 PKYLHYDEETSHQLCDKCPGTYLKQCHTAKWTKVCAPCPDHYTDSWHTSDECLYCSP 85
 QY 65 LCGEREERACHATHNRACRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSNTQOQPC 124
 DB 86 VKELQVVKQECNRTHNRVCECKEGRYLETFCLKHSRCPGPGVQVQAGTPERNTVCKRC 145
 QY 125 PGTRFASSSSSQCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGFFPLSTRVPGAEB--C 182


```
Db 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSSESTQKCGIDVTLC 202
Qy 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 10
US-08-795-445A-6
; Sequence 6, Application US/08795445A
; Patent No. 6284495
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,445A
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-445A-6

Query Match 29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

Qy 5 PTFWRDAETGERLVCAQPGTFFVQRCRDSPTTCGPPRHHTQFWNYLRCRYCNV 64
Db 26 PKYLHYDEETSHQLCDKCPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECLYCSP 85
Qy 65 LCGRESEARACHATHNRACRCTGFFAHAGFCLEHASCPPGAGVIACTPSQNTQCP 124
Db 86 VKELQVYKQECNTHRVCECKEGRYLEIFCLKHSRCPGFGVWQAGTPERNIVCKRC 145
Qy 125 PPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAEE--C 182
Db 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSSESTQKCGIDVTLC 202
Qy 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 11
US-08-795-447A-6
; Sequence 6, Application US/08795447A
; Patent No. 6284723
```

```
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: Osteoprotegerin
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91362-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,447A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Winter, Robert B.
; REFERENCE/DOCKET NUMBER: A-378D2
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 401 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-795-447A-6

Query Match 29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

Qy 5 PTFWRDAETGERLVCAQPGTFFVQRCRDSPTTCGPPRHHTQFWNYLRCRYCNV 64
Db 26 PKYLHYDEETSHQLCDKCPGTYLKQHTAKWTKVCAPCPDHYTDSWHTSDECLYCSP 85
Qy 65 LCGRESEARACHATHNRACRCTGFFAHAGFCLEHASCPPGAGVIACTPSQNTQCP 124
Db 86 VKELQVYKQECNTHRVCECKEGRYLEIFCLKHSRCPGFGVWQAGTPERNIVCKRC 145
Qy 125 PPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAEE--C 182
Db 146 PDGFFSNETSSKAPCRKHTNCSVFGLLLTQKGNATHDNI---CSGNSSESTQKCGIDVTLC 202
Qy 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 12
US-08-794-186-6
; Sequence 6, Application US/08974186
; Patent No. 6284740
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Dehavilland Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-974-186-6

Query Match      29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGTFVQRCRRDPSPTTCGCPRRHYTFQWNYLERCYCNV 64
Db 26 PKYLHYDEETSHQLLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85
QY 65 LCGEREERARACHATHNRACRGTGFEAHAGFCLHASCPCGAGVIAPGTPSONTCQCP 124
Db 86 VKELQYVKQCNRTNHRVCECKEGYLEIEFCLKHSRCPGPGVQAGTPERNIVCKRC 145
QY 125 PPGTFSSASSSEQOPHRNCTALGIALNVPGSSSHDTLCTCTGFPPLSTRVFGAE--C 182
Db 146 PDGFFSNETSSKAPCKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTL 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 13
US-08-795-446B-6
; Sequence 6, Application US/08795446B
; Patent No. 6288032
; GENERAL INFORMATION:
; APPLICANT: Boyle, William J.
; APPLICANT: Lacey, David L.
; APPLICANT: Calzone, Frank J.
; APPLICANT: Chang, Ming-Shi
; TITLE OF INVENTION: OSTEOPROTEGERIN
; NUMBER OF SEQUENCES: 53
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: 1840 Beverlyland Drive
; City: Thousand Oaks
; STATE: California
; COUNTRY: USA
; ZIP: 91320-1789
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/795,446B
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/577,788
```

```
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,186
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/577,788
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Winter, Robert B.
REFERENCE/DOCKET NUMBER: A-378
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-795-446B-6

Query Match      29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGTFVQRCRRDPSPTTCGCPRRHYTFQWNYLERCYCNV 64
Db 26 PKYLHYDEETSHQLLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85
QY 65 LCGEREERARACHATHNRACRGTGFEAHAGFCLHASCPCGAGVIAPGTPSONTCQCP 124
Db 86 VKELQYVKQCNRTNHRVCECKEGYLEIEFCLKHSRCPGPGVQAGTPERNIVCKRC 145
QY 125 PPGTFSSASSSEQOPHRNCTALGIALNVPGSSSHDTLCTCTGFPPLSTRVFGAE--C 182
Db 146 PDGFFSNETSSKAPCKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTL 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 14
US-09-153-927-1
; Sequence 1, Application US/09153927A
; Patent No. 6297022
; GENERAL INFORMATION:
; APPLICANT: McDonnell, Peter C.
; APPLICANT: Young, Peter R.
; APPLICANT: Zou, Jun
; TITLE OF INVENTION: A Method of Identifying Agonists and
; TITLE OF INVENTION: Antagonists for Tumor Necrosis Related Receptors TR1, TR3
; TITLE OF INVENTION: and TR5
; FILE REFERENCE: GH50031
; CURRENT APPLICATION NUMBER: US/09/153,927A
; CURRENT FILING DATE: 1998-09-16
; EARLIER APPLICATION NUMBER: 60/061,334
; EARLIER FILING DATE: 1997-10-08
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: Human
; US-09-153-927-1

Query Match      29.5%; Score 440.5; DB 3; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTYWRDAETGERLVCAQCPGTFVQRCRRDPSPTTCGCPRRHYTFQWNYLERCYCNV 64
Db 26 PKYLHYDEETSHQLLCDKCPGTYLKQCTAKWKTVCAPCPDHYTDSWHTSDECLYCSP 85
QY 65 LCGEREERARACHATHNRACRGTGFEAHAGFCLHASCPCGAGVIAPGTPSONTCQCP 124
Db 86 VKELQYVKQCNRTNHRVCECKEGYLEIEFCLKHSRCPGPGVQAGTPERNIVCKRC 145
QY 125 PPGTFSSASSSEQOPHRNCTALGIALNVPGSSSHDTLCTCTGFPPLSTRVFGAE--C 182
Db 146 PDGFFSNETSSKAPCKHTNCSVFGLLLTQKGNATHDNI---CSGNSESTQKCGIDVTL 202
```

QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

RESULT 15
US-09-072-993C-1
; Sequence 1: Application US/09072993C
; Patent No. 6348388
; GENERAL INFORMATION:
; APPLICANT: Michael R. Brigham--Burke
; APPLICANT: Peter R. Young
; TITLE OF INVENTION: A METHOD OF IDENTIFYING AGONIST AND
; TITLE OF INVENTION: ANTAGONISTS FOR TUMOR NECROSIS RELATED RECEPTORS TRL AND TR2
; FILE REFERENCE: GH-50030
; CURRENT APPLICATION NUMBER: US/09/072,993C
; CURRENT FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/055,513
; PRIOR FILING DATE: 1997-08-13
; PRIOR APPLICATION NUMBER: 60/056,980
; PRIOR FILING DATE: 1997-08-26
; PRIOR APPLICATION NUMBER: 60/057,550
; PRIOR FILING DATE: 1997-08-29
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1
; LENGTH: 401
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-072-993C-1

Query Match 29.5%; Score 440.5; DB 4; Length 401;
Best Local Similarity 41.2%; Pred. No. 4.3e-31;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;
QY 5 PTPWRDAETGERLIVCAQCPPGTFVQRPCCRCSPTTCGCPPPRHYYTQFWNYLRCRYCNV 64
Db 26 PKYLHYDEETSHQLLCCXCPGPGIVLKQHCYAKWKTVCAPCPDHYHTLSWHTSDECLYCSP 85
QY 65 LCGEREERARACHATHNRACRTGTFFAHAGFCLFHASCPPGAGWIAPGTPSQNTQOQC 124
Db 86 VKLEQYVKQECNRTNHRVCECKEGRYLEIEFCLKHSRSCPPFGVGVQAGTPERNTVCKRC 145
QY 125 PGCTESASSSSSCCOPHRCXTALGLALNVPGSSSHDTLCTCTGTFPLSTRVPGAEE--C 182
Db 146 PDGFFSNETSAPCRXHTNCSVFGLLLTQXGNATHDNI---CSGNSESTQKCGIDVTLC 202
QY 183 ERAVIDF 189
Db 203 EEAFFRF 209

Search completed: April 22, 2004, 13:25:47
Job time : 23 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 22, 2004, 13:23:50 ; Search time 48 Seconds

(without alignments)
1560.933 Million cell updates/sec

Title: US-10-069-385-1

Perfect score: 1491

Sequence: 1 VAEPTYPWRDAETGERLVC.....RVAMPGLRSVRERFLVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1133595 seqs, 276475211 residues

Total number of hits satisfying chosen parameters: 1133595

Minimum DB seq length: 3

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

```
1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	271	14	US-10-129-709-1
2	1491	100.0	300	9	US-09-896-096A-1
3	1491	100.0	300	9	US-09-894-924-1
4	1491	100.0	300	9	US-09-935-727-2
5	1491	100.0	300	14	US-10-129-709-3
6	1491	100.0	300	14	US-10-125-985-2
7	1491	100.0	300	15	US-10-310-793-6
8	1491	100.0	300	15	US-10-369-300-19
9	1491	100.0	300	15	US-10-375-680-52
10	1491	100.0	300	15	US-10-418-242-2
11	1491	100.0	300	15	US-10-456-819-1
12	1491	100.0	341	14	US-10-106-698-4514
13	1476.5	99.0	299	9	US-09-877-156-17
14	4469	98.5	300	9	US-09-840-735-2
15	1389	93.2	326	15	US-10-264-049-3112

16	1034	69.3	211	9	US-09-877-156-20	Sequence 20, Appl
17	855	57.3	146	15	US-10-375-680-59	Sequence 59, Appl
18	841	56.4	153	9	US-09-877-156-2	Sequence 2, Appl
19	671	45.0	170	9	US-09-935-727-4	Sequence 4, Appl
20	671	45.0	170	15	US-10-418-242-4	Sequence 4, Appl
21	461	30.9	326	9	US-09-062-113-71	Sequence 71, Appl
22	461	30.9	326	14	US-10-232-858-71	Sequence 71, Appl
23	442.5	29.7	401	9	US-09-062-113-62	Sequence 62, Appl
24	442.5	29.7	401	14	US-10-232-858-62	Sequence 62, Appl
25	440.5	29.5	272	9	US-09-062-113-75	Sequence 75, Appl
26	440.5	29.5	272	14	US-10-232-858-75	Sequence 75, Appl
27	440.5	29.5	293	9	US-09-896-096A-18	Sequence 18, Appl
28	440.5	29.5	293	9	US-09-894-924-18	Sequence 18, Appl
29	440.5	29.5	293	15	US-10-456-819-18	Sequence 18, Appl
30	440.5	29.5	321	9	US-09-062-113-80	Sequence 80, Appl
31	440.5	29.5	321	14	US-10-232-858-80	Sequence 80, Appl
32	440.5	29.5	327	9	US-09-062-113-72	Sequence 72, Appl
33	440.5	29.5	327	14	US-10-232-858-72	Sequence 72, Appl
34	440.5	29.5	349	12	US-10-105-934-15	Sequence 15, Appl
35	440.5	29.5	351	9	US-09-062-113-74	Sequence 74, Appl
36	440.5	29.5	351	14	US-10-232-858-74	Sequence 74, Appl
37	440.5	29.5	362	9	US-09-062-113-11	Sequence 11, Appl
38	440.5	29.5	362	14	US-10-232-858-11	Sequence 11, Appl
39	440.5	29.5	380	9	US-09-062-113-4	Sequence 4, Appl
40	440.5	29.5	380	11	US-09-405-032-139	Sequence 139, App
41	440.5	29.5	380	14	US-10-232-858-4	Sequence 4, Appl
42	440.5	29.5	390	14	US-10-155-167-2	Sequence 2, Appl
43	440.5	29.5	391	9	US-09-062-113-106	Sequence 106, App
44	440.5	29.5	391	14	US-10-232-858-106	Sequence 106, App
45	440.5	29.5	393	9	US-09-062-113-79	Sequence 79, Appl

ALIGNMENTS

RESULT 1
US-10-129-709-1
; Sequence 1, Application US/10129709
; Publication No. US20030055221A1
; GENERAL INFORMATION:
; APPLICANT: Witicher, Derrick
; APPLICANT: Lu, Jirong
; TITLE OF INVENTION: Improving stability of FLINT through O-linked glycosylation
; FILE REFERENCE: X-13531M
; CURRENT APPLICATION NUMBER: US/10/129,709
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 1
; LENGTH: 271
; TYPE: PNT
; ORGANISM: Homo sapiens
US-10-129-709-1

Query Match 100.0%; Score 1491; DB 14; Length 271;
Best Local Similarity 100.0%; Pred. No. 7.4e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	VAEPTYPWRDAETGERLVCACQPGTTFVQRCRDSPTTCGCPPHRYTQWNYLCRCR	60
DB	1	VAEPTYPWRDAETGERLVCACQPGTTFVQRCRDSPTTCGCPPHRYTQWNYLCRCR	60
QY	61	YCNVLCGRREERACHATHNACRCRTGFFAHAGFCLEHASCPCGAGVIAGTFSQNTQ	120
DB	61	YCNVLCGRREERACHATHNACRCRTGFFAHAGFCLEHASCPCGAGVIAGTFSQNTQ	120
QY	121	CQCPGPTFSASSSSSEQCPHRNCTALGLALNVPGSSSHDLTCTSGTGFPLSTRVPGAE	180
DB	121	CQCPGPTFSASSSSSEQCPHRNCTALGLALNVPGSSSHDLTCTSGTGFPLSTRVPGAE	180
QY	181	ECERAVIDFVAFODISIKELQLLQALEAPEGWGTPPRAGRAALQKLRRLTELGAOD	240
DB	181	ECERAVIDFVAFODISIKELQLLQALEAPEGWGTPPRAGRAALQKLRRLTELGAOD	240

QY 241 GALLVRLQALRVARMPGLSVRRERFLPVH 271
 DE 241 GALLVRLQALRVARMPGLSVRRERFLPVH 271

RESULT 2

US-09-896-096A-1
 ; Sequence 1, Application US/09896096A
 ; Patent No. US20020061559A1

GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J
 ; APPLICANT: BOSTEIN, DAVID
 ; APPLICANT: DODGE, KELLY H.
 ; APPLICANT: GURNEY, AUSTIN L.
 ; APPLICANT: KIM, KYUNG JIN
 ; APPLICANT: LAWRENCE, DAVID A.
 ; APPLICANT: PITTI, ROBERT
 ; APPLICANT: ROY, MARGARET A
 ; APPLICANT: TUMAS, DANIEL B
 ; APPLICANT: WOOD, WILLIAM I.

; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
 ; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/09/896,096A

; CURRENT FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 1

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-09-896-096A-1

Query Match 100.0%; Score 1491; DB 9; Length 300;
 Best Local Similarity 100.0%; Pred. No. 8.3e-116;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGPPRRHYTQFWNYLRCR 60
 DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGPPRRHYTQFWNYLRCR 89
 QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120
 DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 149
 QY 121 CQCPGPTFSASSSSSEQPHNCTALGLALNVPSSSHDILCTCTGFPPLSTRVPGAE 180
 DB 150 CQCPGPTFSASSSSSEQPHNCTALGLALNVPSSSHDILCTCTGFPPLSTRVPGAE 209
 QY 181 ECERAVIDVAFODISIKRLQLQALAEFEGMGPTPRAGRAALQKLRRLTELLGAQD 240
 DB 210 ECERAVIDVAFODISIKRLQLQALAEFEGMGPTPRAGRAALQKLRRLTELLGAQD 269
 QY 241 GALLVRLQALRVARMPGLSVRRERFLPVH 271
 DB 270 GALLVRLQALRVARMPGLSVRRERFLPVH 300

RESULT 3

US-09-894-924-1
 ; Sequence 1, Application: US/09894924
 ; Patent No. US20020065210A1

GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J
 ; APPLICANT: BOSTEIN, DAVID
 ; APPLICANT: DODGE, KELLY H.
 ; APPLICANT: GURNEY, AUSTIN L.
 ; APPLICANT: KIM, KYUNG JIN

; APPLICANT: LAWRENCE, DAVID A.
 ; APPLICANT: PITTI, ROBERT
 ; APPLICANT: ROY, MARGARET A
 ; APPLICANT: TUMAS, DANIEL B
 ; APPLICANT: WOOD, WILLIAM I.
 ; TITLE OF INVENTION: DCR3 Polypeptide, A TNFR Homolog
 ; FILE REFERENCE: P1134R2 REVISED
 ; CURRENT APPLICATION NUMBER: US/09/894,924
 ; CURRENT FILING DATE: 2001-06-28
 ; PRIOR APPLICATION NUMBER: US 09/157,289
 ; PRIOR FILING DATE: 1998-09-18
 ; PRIOR APPLICATION NUMBER: US 60/059,288
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: US 60/094,640
 ; PRIOR FILING DATE: 1998-07-30
 ; NUMBER OF SEQ ID NOS: 18
 ; SEQ ID NO 1
 ; LENGTH: 300
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-894-924-1

Query Match 100.0%; Score 1491; DB 9; Length 300;
 Best Local Similarity 100.0%; Pred. No. 8.3e-116;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGPPRRHYTQFWNYLRCR 60
 DB 30 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGPPRRHYTQFWNYLRCR 89
 QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120
 DB 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 149
 QY 121 CQCPGPTFSASSSSSEQPHNCTALGLALNVPSSSHDILCTCTGFPPLSTRVPGAE 180
 DB 150 CQCPGPTFSASSSSSEQPHNCTALGLALNVPSSSHDILCTCTGFPPLSTRVPGAE 209
 QY 181 ECERAVIDVAFODISIKRLQLQALAEFEGMGPTPRAGRAALQKLRRLTELLGAQD 240
 DB 210 ECERAVIDVAFODISIKRLQLQALAEFEGMGPTPRAGRAALQKLRRLTELLGAQD 269
 QY 241 GALLVRLQALRVARMPGLSVRRERFLPVH 271
 DB 270 GALLVRLQALRVARMPGLSVRRERFLPVH 300

RESULT 4

US-09-935-727-2
 ; Sequence 2, Application US/09935727
 ; Patent No. US20020150583A1

GENERAL INFORMATION:

; APPLICANT: Human Genome Sciences, Inc.
 ; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta
 ; FILE REFERENCE: PF454P2
 ; CURRENT APPLICATION NUMBER: US/09/935,727
 ; CURRENT FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: 60/303,224
 ; PRIOR FILING DATE: 2001-07-06
 ; PRIOR APPLICATION NUMBER: 60/252,131
 ; PRIOR FILING DATE: 2000-11-21
 ; PRIOR APPLICATION NUMBER: 60/227,598
 ; PRIOR FILING DATE: 2000-08-25
 ; PRIOR APPLICATION NUMBER: 09/518,931
 ; PRIOR FILING DATE: 2000-03-03
 ; PRIOR APPLICATION NUMBER: 60/168,235
 ; PRIOR FILING DATE: 1999-12-01
 ; PRIOR APPLICATION NUMBER: 60/146,371
 ; PRIOR FILING DATE: 1999-08-02
 ; PRIOR APPLICATION NUMBER: 60/131,964
 ; PRIOR FILING DATE: 1999-04-30
 ; PRIOR APPLICATION NUMBER: 60/131,270
 ; PRIOR FILING DATE: 1999-04-27

```

; PRIOR APPLICATION NUMBER: 60/124,092
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/121,774
; PRIOR FILING DATE: 1999-03-04
; PRIOR APPLICATION NUMBER: 09/006,352
; PRIOR FILING DATE: 1998-01-13
; PRIOR APPLICATION NUMBER: 60/035,496
; PRIOR FILING DATE: 1997-01-14
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-935-727-2

Query Match 100.0%; Score 1491; DB 9; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 120
DB 90 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 149
QY 121 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180
DB 150 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 209
QY 181 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
DB 210 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQALRVARMPLGLSVRERFLPVH 271
DB 270 GALLVRLQALRVARMPLGLSVRERFLPVH 300

RESULT 5
US-10-129-709-3
; Sequence 3, Application US/10129709
; Publication No. US2003005522A1
; GENERAL INFORMATION:
; APPLICANT: Wittecher, Derrick
; APPLICANT: Lu, Jirong
; TITLE OF INVENTION: Improving stability of FLINT through O-linked glycosylation
; FILE REFERENCE: X-13531M
; CURRENT APPLICATION NUMBER: US/10/129,709
; CURRENT FILING DATE: 2002-05-07
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 3
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-129-709-3

Query Match 100.0%; Score 1491; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 120
DB 90 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 149
QY 121 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180

```

```

DB 150 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 209
QY 181 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
DB 210 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQALRVARMPLGLSVRERFLPVH 271
DB 270 GALLVRLQALRVARMPLGLSVRERFLPVH 300

RESULT 6
US-10-125-985-2
; Sequence 2, Application US/10125985
; Publication No. US20030166158A1
; GENERAL INFORMATION:
; APPLICANT: Hsu, Hailing
; TITLE OF INVENTION: NTR3 A No. US20030166158A1 Member of the TNF-Receptor Supergene
; FILE REFERENCE: D1617/35549A
; CURRENT APPLICATION NUMBER: US/10/125,985
; CURRENT FILING DATE: 2002-04-19
; PRIOR APPLICATION NUMBER: US/09/632,277A
; PRIOR FILING DATE: 2000-08-03
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-125-985-2

Query Match 100.0%; Score 1491; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 60
DB 30 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSFTTCGPPRRHYTQFWNYLERCR 89
QY 61 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 120
DB 90 YCNVLCGEREEERACHATHNRCRTGTFFAHAGFCLHASCPPGAGVIAPGTPSNTQ 149
QY 121 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 180
DB 150 CQPCPPGTFSSASSSSQCPHNRCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGA 209
QY 181 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
DB 210 ECRVIDFVAFODISIKRLQRLQALEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQALRVARMPLGLSVRERFLPVH 271
DB 270 GALLVRLQALRVARMPLGLSVRERFLPVH 300

RESULT 7
US-10-310-793-6
; Sequence 6, Application US/10310793
; Publication No. US20030198640A1
; GENERAL INFORMATION:
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ni, Jian
; APPLICANT: Rosen, Craig A
; APPLICANT: Zhang, Jun
; APPLICANT: Wei, Ping
; TITLE OF INVENTION: Methods and Compositions For Treating Inflammatory Bowel Diseases
; TITLE OF INVENTION: Relating to Human Tumor Necrosis Factor-Gamma Beta
; FILE REFERENCE: P573
; CURRENT APPLICATION NUMBER: US/10/310,793
; CURRENT FILING DATE: 2002-12-06

```

```
; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PAMM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 300
; TYPE: ERT
; ORGANISM: human
US-10-310-793-6

Query Match      100.0%; Score 1491; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 60
Db 30 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 89
QY 61 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 120
Db 90 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 149
QY 121 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
Db 150 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
Db 210 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
Db 270 GALLVRLQLALRVARMPGLERSVRERFLPVH 300

RESULT 9
US-10-375-680-52
; Sequence 52, Application US/10375680
; Publication No. US20040009147A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; APPLICANT: Yu, Guo-Liang
; APPLICANT: Ruben, Steven M
; APPLICANT: Ullrich, Stephen
; APPLICANT: Zhai, Yifan
; TITLE OF INVENTION: Apoptosis Inducing Molecule II and Methods of Use
; FILE REFERENCE: 1489.065000E
; CURRENT APPLICATION NUMBER: US/10/375,680
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,234
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 70
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 52
; LENGTH: 300
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-375-680-52

Query Match      100.0%; Score 1491; DB 15; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 60
Db 30 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 89
QY 61 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 120
Db 90 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 149
QY 121 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
Db 150 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
Db 210 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 269

; PRIOR APPLICATION NUMBER: 60/336,695
; PRIOR FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 10/226,294
; PRIOR FILING DATE: 2002-08-23
; PRIOR APPLICATION NUMBER: 60/314,381
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: 09/899,059
; PRIOR FILING DATE: 2001-07-06
; PRIOR APPLICATION NUMBER: 60/278,449
; PRIOR FILING DATE: 2001-03-26
; PRIOR APPLICATION NUMBER: 60/216,879
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: 09/559,290
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/180,908
; PRIOR FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 60/134,067
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: 60/132,227
; PRIOR FILING DATE: 1999-05-03
; Remaining Prior Application data removed - See File Wrapper or PAMM.
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 300
; TYPE: ERT
; ORGANISM: human
US-10-310-793-6

Query Match      100.0%; Score 1491; DB 14; Length 300;
Best Local Similarity 100.0%; Pred. No. 8.3e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 60
Db 30 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSTTCGPPRHVYTFQWNYLERCR 89
QY 61 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 120
Db 90 YCNVLCGEREREACHATHNRACRGTGFFAHAGFCLFHASCPCPGAGVIAFGTFSQNTQ 149
QY 121 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 180
Db 150 COPCPPTGFSASSSSSEQCPHRNCTALGLALNVPGSSSHDTLCTSGTGFPLSTRVPGAE 209
QY 181 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 240
Db 210 ECERAVIDFVAFQDISIKRLQLQALEAPEGWGPTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQLALRVARMPGLERSVRERFLPVH 271
Db 270 GALLVRLQLALRVARMPGLERSVRERFLPVH 300

RESULT 8
US-10-369-300-19
; Sequence 19, Application US/1036930C
; Publication No. US20030215442A1
; GENERAL INFORMATION:
; APPLICANT: Fraser, Christopher
; APPLICANT: Hancock, Wayne
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE TREATMENT OR PREVENTION OF
; TITLE OF INVENTION: IMMUNE
; TITLE OF INVENTION: DISORDERS USING COMBINATION THERAPY
; FILE REFERENCE: 7853-255
; CURRENT APPLICATION NUMBER: US/10/369,300
; CURRENT FILING DATE: 2003-02-19
; PRIOR APPLICATION NUMBER: 60/358,463
; PRIOR FILING DATE: 2002-02-19
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 19
; LENGTH: 300
```


QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271
 |||||
 Db 270 GALLVRLQLALRVARMPGLERSVREERFLPVH 300

RESULT 10

US-10-418-242-2

; Sequence 2, Application US/10418242

; Publication No. US20040013664A1

; GENERAL INFORMATION:

; APPLICANT: Gentz et al.

; TITLE OF INVENTION: Tumor Necrosis Factor Receptors 6 Alpha and 6 Beta

; FILE REFERENCE: PF454F3

; CURRENT APPLICATION NUMBER: US/10/418,242

; PRIOR FILING DATE: 2003-04-18

; PRIOR APPLICATION NUMBER: 60/373,604

; PRIOR FILING DATE: 2002-04-19

; PRIOR APPLICATION NUMBER: 09/935,727

; PRIOR FILING DATE: 2001-08-24

; PRIOR APPLICATION NUMBER: 60/303,224

; PRIOR FILING DATE: 2001-07-06

; PRIOR APPLICATION NUMBER: 60/252,131

; PRIOR FILING DATE: 2000-11-21

; PRIOR APPLICATION NUMBER: 60/227,593

; PRIOR FILING DATE: 2000-08-25

; PRIOR APPLICATION NUMBER: 09/518,931

; PRIOR FILING DATE: 2000-03-03

; PRIOR APPLICATION NUMBER: 60/168,235

; PRIOR FILING DATE: 1999-12-01

; PRIOR APPLICATION NUMBER: 60/146,371

; PRIOR FILING DATE: 1999-08-02

; PRIOR APPLICATION NUMBER: 60/131,964

; PRIOR FILING DATE: 1999-04-30

; PRIOR APPLICATION NUMBER: 60/131,273

; PRIOR FILING DATE: 1999-04-27

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 51

; SEQ ID NO 2

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-418-242-2

Query Match 100.0%; Score 1491; DB 15; Length 300;

Best Local Similarity 100.0%; Pred. No. 8.3e-116;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPGGTFVORPCRRDSPTTCGCPGPPRHYTQFWNYLERCR 60

|||

Db 30 VAEPTYPWRDAETGERLVCAQCPGGTFVORPCRRDSPTTCGCPGPPRHYTQFWNYLERCR 89

QY 61 YCNVLCGEREEERARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120

|||

Db 90 YCNVLCGEREEERARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 149

QY 121 CQPCPGTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180

|||

Db 150 CQPCPGTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 209

QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGCGPTPRAGRAALQLKRLRELTLLGAQD 240

|||

Db 210 ECERAVIDFVAFODISIKRLQRLQALEAPEGCGPTPRAGRAALQLKRLRELTLLGAQD 269

QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

|||

Db 270 GALLVRLQLALRVARMPGLERSVREERFLPVH 300

RESULT 11

US-10-456-819-1

; Sequence 1, Application US/10456819

; Publication No. US20040014176A1

; GENERAL INFORMATION:

; APPLICANT: ASHKENAZI, AVI J
 ; APPLICANT: BOTSTEIN, DAVID
 ; APPLICANT: DODGE, KELLY H.
 ; APPLICANT: GURNEY, AUSTIN L.
 ; APPLICANT: KIM, KYUNG JIN
 ; APPLICANT: LAWRENCE, DAVID A.
 ; APPLICANT: PITTL, ROBERT
 ; APPLICANT: ROY, MARGARET A
 ; APPLICANT: TOMAS, DANIEL B
 ; APPLICANT: WOOD, WILLIAM I.
 ; TITLE OF INVENTION: Dcr3 Polypeptide, A TNFR Homolog

; FILE REFERENCE: P1134R2 REVISED

; CURRENT APPLICATION NUMBER: US/10/456,819

; CURRENT FILING DATE: 2003-06-06

; PRIOR APPLICATION NUMBER: US/09/894,924

; PRIOR FILING DATE: 2001-06-28

; PRIOR APPLICATION NUMBER: US 09/157,289

; PRIOR FILING DATE: 1998-09-18

; PRIOR APPLICATION NUMBER: US 60/059,288

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: US 60/094,640

; PRIOR FILING DATE: 1998-07-30

; NUMBER OF SEQ ID NOS: 18

; SEQ ID NO 1

; LENGTH: 300

; TYPE: PRT

; ORGANISM: Homo sapiens

US-10-456-819-1

Query Match 100.0%; Score 1491; DB 15; Length 300;

Best Local Similarity 100.0%; Pred. No. 8.3e-116;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAEPTYPWRDAETGERLVCAQCPGGTFVORPCRRDSPTTCGCPGPPRHYTQFWNYLERCR 60

|||

Db 30 VAEPTYPWRDAETGERLVCAQCPGGTFVORPCRRDSPTTCGCPGPPRHYTQFWNYLERCR 89

QY 61 YCNVLCGEREEERARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 120

|||

Db 90 YCNVLCGEREEERARACHATHNACRCRTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQ 149

QY 121 CQPCPGTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 180

|||

Db 150 CQPCPGTFSASSSSSQCPHNRCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVPGAE 209

QY 181 ECERAVIDFVAFODISIKRLQRLQALEAPEGCGPTPRAGRAALQLKRLRELTLLGAQD 240

|||

Db 210 ECERAVIDFVAFODISIKRLQRLQALEAPEGCGPTPRAGRAALQLKRLRELTLLGAQD 269

QY 241 GALLVRLQLALRVARMPGLERSVREERFLPVH 271

|||

Db 270 GALLVRLQLALRVARMPGLERSVREERFLPVH 300

RESULT 12

US-10-106-698-4514

; Sequence 4514, Application US/10106698

; Publication No. US20030109690A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptides

; FILE REFERENCE: PA005P1

; CURRENT APPLICATION NUMBER: US/10/106,698

; CURRENT FILING DATE: 2002-03-27

; PRIOR APPLICATION NUMBER: PCT/US00/26524

; PRIOR FILING DATE: 2000-09-28

; PRIOR APPLICATION NUMBER: US 60/157,137

; PRIOR FILING DATE: 1999-09-29

; PRIOR APPLICATION NUMBER: US 60/163,280

; PRIOR FILING DATE: 1999-11-03

; NUMBER OF SEQ ID NOS: 8564

; SOFTWARE: PatentIn Ver. 3.0

; SEQ ID NO 4514

```
; LENGTH: 34;
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-106-598-4514

Query Match      100.0%; Score 1491; DB 14; Length 341;
Best Local Similarity 100.0%; Pred. No. 9.6e-116;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 60
Db 71 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 130
QY 61 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
Db 131 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 190
QY 121 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 180
Db 191 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 250
QY 181 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
Db 251 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 310
QY 241 GALLVRLQALRVARMMPGLERSVRERFLPVH 271
Db 311 GALLVRLQALRVARMMPGLERSVRERFLPVH 341

RESULT 13
US-09-877-156-17
; Sequence 17, Application US/09877156
; Patent No. US20020055625A1
; GENERAL INFORMATION:
; APPLICANT: Catherine Tribouley
; TITLE OF INVENTION: NEW MEMBERS OF TNE AND TNER FAMILIES
; FILE REFERENCE: 1408.003/200130.439C1
; CURRENT APPLICATION NUMBER: US/09/877,156
; PRIOR FILING DATE: 2001-06-08
; PRIOR APPLICATION NUMBER: US 09/286,529
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 299
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-877-156-17

Query Match      99.0%; Score 1476.5; DB 9; Length 299;
Best Local Similarity 99.6%; Pred. No. 1.3e-114;
Matches 270; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 60
Db 30 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 89
QY 61 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
Db 90 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 180
Db 150 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 208
QY 181 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
Db 209 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 268
QY 241 GALLVRLQALRVARMMPGLERSVRERFLPVH 271
Db 269 GALLVRLQALRVARMMPGLERSVRERFLPVH 299
```

```
RESULT 14
US-09-843-795-2
; Sequence 2, Application US/09840795
; Patent No. US20020143147A1
; GENERAL INFORMATION:
; APPLICANT: Murphy, Erin E.
; APPLICANT: Mattson, Jeanine D.
; APPLICANT: Bates, Elizabeth Esther Mary
; APPLICANT: Gorman, Daniel M.
; APPLICANT: Lebecque, Serge J.E.
; TITLE OF INVENTION: Mammalian Genes; Related Reagents
; FILE REFERENCE: SF3818K
; CURRENT APPLICATION NUMBER: US/09/840,795
; CURRENT FILING DATE: 2001-04-23
; PRIOR APPLICATION NUMBER: 09/351,777
; PRIOR FILING DATE: 1999-07-12
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 300
; TYPE: PRT
; ORGANISM: primate
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: {79}
; OTHER INFORMATION: Xaa at residue 79 is undetermined.
US-09-840-795-2

Query Match      98.5%; Score 1469; DB 9; Length 300;
Best Local Similarity 98.9%; Pred. No. 5.6e-114;
Matches 268; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 60
Db 30 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDSTTCGCPPRHYTQFWNYLRCR 89
QY 61 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 120
Db 90 YCNVLCGEREEERACHATHNRACRTGFFAHAGFCLEHASCPPGAGVIAPGTPSQNTQ 149
QY 121 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 180
Db 150 CQCPGPGTFSSASSSSQCPHRNCTALGLALNVPGSSSHDTLCTSCGFFLSTVRPGAE 209
QY 181 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 240
Db 210 ECERAVIDFVAFQDISIKRLQRLQALAEAPGEGWGTTPRAGRAALQKLRRRLTELLGAQD 269
QY 241 GALLVRLQALRVARMMPGLERSVRERFLPVH 271
Db 270 GALLVRLQALRVARMMPGLERSVRERFLPVH 300

RESULT 15
US-10-264-049-3112
; Sequence 3112, Application US/10264049
; Publication No. US20040005579A1
; GENERAL INFORMATION:
; APPLICANT: Birse et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P4133P1
; CURRENT APPLICATION NUMBER: US/10/264,049
; CURRENT FILING DATE: 2002-10-04
; PRIOR APPLICATION NUMBER: PCT/US01/18569
; PRIOR FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: US 60/209,467
; PRIOR FILING DATE: 2000-06-07
; NUMBER OF SEQ ID NOS: 4360
; SOFTWARE: PatentIn Ver. 3.1
; SEQ ID NO 3112
; LENGTH: 326
```

```
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-264-043-3112
Query Match      93.2%; Score 1389; DB 15; Length 326;
Best Local Similarity 99.8%; Pred No. 2.7e-107;
Matches 251; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 VAETPTYEMRDAETGERLVCAQCPPGTFVORPCRRDSPPTTCGECPPRHYYTQFWNYLERCR 60
Db 54 VAETPTYPWRDAETGERLVCAQCPPGTFVORPCRRDSPPTTCGECPPRHYYTQFWNYLERCR 123
QY 61 YCNVLCGEREEERACHATENRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTQ 120
Db 124 YCNVLCGEREEERACHATENRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSONTQ 183
QY 121 CQCPPTGTFSSASSSSSEOCOPHNCTALGLALNVPSSSSHDTLCTSGTGFPLSTRVEGAE 180
Db 184 CQCPPTGTFSSASSSSSEOCOPHNCTALGLALNVPSSSSHDTLCTSGTGFPLSTRVEGAE 243
QY 181 ECERAVIDFVAFODISIKRLQRLLOALEAPEGNGPTPRAGRAALQLKLRRLTELLGAQD 240
Db 244 ECERAVIDFVAFODISIKRLQRLLOALEAPEGNGPTPRAGRAALQLKLRRLTELLGAQD 303
QY 241 GALLVELLQALR 252
Db 304 GALLVELLQAAAR 315
```

Search completed: April 22, 2004, 13:33:17
Job time : 49 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2003, 13:07:01; Search time 41 Seconds

(without alignments)
1049.144 Million cell updates/sec

Title: US-10-069-385-1

Perfect score: 1491

Sequence: 1 VAEPTYPMDAETGERLVC.....RVAMPGLERSVRRPLPVH 271

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A Geneseq 19Jun03;*

1: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1980.DAT:*

2: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1981.DAT:*

3: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1982.DAT:*

4: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1983.DAT:*

5: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1984.DAT:*

6: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1985.DAT:*

7: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1986.DAT:*

8: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1987.DAT:*

9: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1988.DAT:*

10: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1989.DAT:*

11: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1990.DAT:*

12: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1991.DAT:*

13: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1992.DAT:*

14: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1993.DAT:*

15: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1994.DAT:*

16: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1995.DAT:*

17: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1996.DAT:*

18: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1997.DAT:*

19: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1998.DAT:*

20: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA1999.DAT:*

21: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2000.DAT:*

22: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2001.DAT:*

23: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2002.DAT:*

24: /SIDSL/gcgdata/geneseq/geneseq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	100.0	271	20	Human mFLINT #1 pr
2	1491	100.0	271	21	A mature human FAS
3	1491	100.0	271	21	Human FAS ligand i
4	1491	100.0	271	21	M68 TNF receptor r
5	1491	100.0	271	21	Human mature FLINT
6	1491	100.0	271	22	Human mature fas l
7	1491	100.0	271	22	Amino acid sequenc
8	1491	100.0	271	22	Amino acid sequenc
9	1491	100.0	271	22	Human FLINT mature

10	1491	100.0	271	23	AAO18767	Human FLINT mature
11	1491	100.0	271	23	ABW75621	Human Fas ligand i
12	1491	100.0	271	23	AAE14578	Human mature FLINT
13	1491	100.0	300	19	AAW66102	Amino acid sequenc
14	1491	100.0	300	19	AAW63622	Human tumour necro
15	1491	100.0	300	20	AAW53099	Human lung TNF-rec
16	1491	100.0	300	20	AAW42182	Human FLINT #1 pro
17	1491	100.0	300	20	AAW17479	Xamalian tumour n
18	1491	100.0	300	20	AAW16817	Human DCR3 polypep
19	1491	100.0	300	20	AAW97749	Human tumour necro
20	1491	100.0	300	20	AAW95082	Orphan receptor (H
21	1491	100.0	300	21	AAW19335	A full length huma
22	1491	100.0	300	21	AAW28559	Human soluble TNF
23	1491	100.0	300	21	AAW24057	Human PRO212 prote
24	1491	100.0	300	21	AAW33416	Human PRO212 prote
25	1491	100.0	300	21	AAW33416	Human Fas ligand i
26	1491	100.0	300	21	AAW33416	Human Fas ligand i
27	1491	100.0	300	21	AAW97246	M68 TNF receptor r
28	1491	100.0	300	21	AAW90357	Human tumour necro
29	1491	100.0	300	21	AAW24395	Human PRO212 prote
30	1491	100.0	300	21	AAW96596	Human FLINT. Homo
31	1491	100.0	300	22	AAW74466	Human native fas l
32	1491	100.0	300	22	AAW71754	Human NTR3. Homo
33	1491	100.0	300	22	AAW48161	Human PRO212 polyp
34	1491	100.0	300	22	AAW50903	Human PRO212 prote
35	1491	100.0	300	23	AAO18768	Human FLINT protei
36	1491	100.0	300	23	ABW79622	Human Fas ligand i
37	1491	100.0	300	23	AAE14579	Human native FLINT
38	1491	100.0	300	23	AAE20848	Human tumour necro
39	1491	100.0	341	22	AAW73740	Human colon cancer
40	1487	99.7	271	21	AAW19709	Protease-resistant
41	1487	99.7	271	22	AAW33571	Human mature fas l
42	1487	99.7	271	22	AAW74467	Human FLINT mature
43	1487	99.7	271	22	AAE14581	Human protease-res
44	1486	99.7	271	22	AAE03584	Human mature fas l
45	1486	99.7	271	23	AAE14582	Human protease-res

ALIGNMENTS

RESULT 1
AAW42184
ID AAW42184 standard; Protein; 271 AA.

XX AAW42184;

XX 17-DEC-1999 (first entry)

XX Human mFLINT #1 protein sequence.

XX Human; FLINT; mFLINT; OPG3; tumour necrosis factor receptor; FasL;
KW apoptosis; inflammation; cancer; diabetes; acute liver failure;
KW sepsis; hepatitis; ischaemia-associated injury; hypercoagulation;
KW reperfusion-associated injury; aplastic anaemia; differentiation;
KW growth; myelodysplastic syndrome; pancytopenic condition;
KW myocardial ischaemia.

XX Homo sapiens.

XX WO9950413-A2.

XX 07-OCT-1999.

XX 30-MAR-1999; 99WO-US06797.

XX 30-MAR-1998; 98US-0079856.

XX 20-MAY-1998; 98US-0086074.

XX 09-SEP-1998; 98US-0096643.

XX 17-DEC-1998; 98US-0112577.

XX 18-DEC-1998; 98US-0112703.

XX 18-DEC-1998; 98US-0112933.

XX 22-DEC-1998; 98US-0113407.

XX PA (ELIL) LILLY & CO ELI.

XX PI Burcol TP, Dou S, Glasebrook AL, Gould KE, Hale JE, Heuer JG;
 XX PI Hui XY, Kharitonov A, Mizrahi J, Na S, Noblitt TW, Reidy CA;
 XX PI Song HY, Wang J, Wu X, Zuckerman SH;
 DR DR WP: 1999-591319/50.
 DR N-PSDB; AAZ25377.

XX XX Use of mature FLINT for treating acute liver failure, inflammation,
 PT cancer, and diabetes - by prevention of FasL-Fas mediated apoptotic
 PT and proinflammatory activity

XX PS Claim 31; Fig 3; 99pp; English.

XX CC The present invention describes therapeutic applications of mature FLINT
 CC (=FLINT) for use in the treatment of acute liver failure. Mature FLINT
 CC (=FLINT), which is a member of the tumour necrosis factor receptor
 CC superfamily, is used for treating acute liver failure, inflammation of
 CC the liver, abnormal hepatocyte apoptosis, sepsis, a disorder associated
 CC with inflammation, hepatitis, abnormal apoptosis, an ischaemia-associated
 CC injury or disorder such as hypercoagulation (including use with
 CC thrombolytic or anti-thrombolytic agents), reperfusion-associated injury
 CC or disorder, Type I diabetes, cancer, cell damage or damage to an
 CC innocent bystander tissue that is induced by a chemotherapeutic agent or
 CC therapeutic irradiation, treating haematopoietic progenitor cells that
 CC have been exposed to therapeutic radiation or chemotherapy, aplastic
 CC anaemia, myelodysplastic syndrome or a pancytopenic condition. FLINT is
 CC also used for promoting the growth or differentiation of a haematopoietic
 CC progenitor cell or CD34+ cell and preventing damage to a cardiac myocyte
 CC resulting from abnormal myocardial ischaemia. The present sequence
 CC represents human mFLINT.

XX SQ Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 20; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VASTPTVPRDAETGERLVCAQCPGGTFVQRPDRDSPTTCGPPRRHYTFQFWNYLERCR 60
 Db |||||
 QY 1 VASTPTVPRDAETGERLVCAQCPGGTFVQRPDRDSPTTCGPPRRHYTFQFWNYLERCR 60
 Db |||||
 QY 61 YCNVLGGEREEERACHATENRACRTGFFAHAGFCLEHASCPGAGVAPGTPSNTQ 120
 Db |||||
 QY 61 YCNVLGGEREEERACHATENRACRTGFFAHAGFCLEHASCPGAGVAPGTPSNTQ 120
 Db |||||
 QY 121 CQPCPGTFSASSSSSQCPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVFGAE 180
 Db |||||
 QY 121 CQPCPGTFSASSSSSQCPHRNCTALGLALNVPGSSSHDTLCTCTGFPPLSTRVFGAE 180
 Db |||||
 QY 181 ECEKAVIDVAFQDISIKRLQLLQALAEFGNGPTPRAGAAQLKLRRLTELLGAQD 240
 Db |||||
 QY 181 ECEKAVIDVAFQDISIKRLQLLQALAEFGNGPTPRAGAAQLKLRRLTELLGAQD 240
 Db |||||
 QY 241 GALLVRLQLARVARMPGLERSVRERFLPVH 271
 Db |||||
 QY 241 GALLVRLQLARVARMPGLERSVRERFLPVH 271
 Db |||||

RESULT 2

AAAB19334

ID AAB-9334 standard; Protein; 271 AA.

XX AC AAB-9334;

XX XX

DT 19-FEB-2001 (first entry)

XX XX

DE A mature human FAS Ligand Inhibitory Protein (FLINT).

XX XX

KW Human; FAS Ligand Inhibitory Protein; FLINT; analogue; apoptosis;
 KW tumour necrosis factor receptor; acute lung injury; pulmonary fibrosis;

KW acute respiratory distress syndrome; ulcerative colitis;
 XX chronic obstructive pulmonary disease; Crohn's disease.

OS Homo sapiens.

XX Key Location/Qualifiers

FT Misc-difference 1 /note= "optionally replaced with Met"
 FT FT
 FT Misc-difference 2 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 4 /note= "optionally replaced with Ala"
 FT FT
 FT Misc-difference 12 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 13 /note= "optionally replaced with Asp or Gln"
 FT FT
 FT Misc-difference 17 /note= "optionally replaced with Trp"
 FT FT
 FT Misc-difference 25 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 34 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 35 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 36 /note= "optionally replaced with Thr"
 FT FT
 FT Misc-difference 37 /note= "optionally replaced with Asn or Thr"
 FT FT
 FT Misc-difference 38 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 53 /note= "optionally replaced with Asp"
 FT FT
 FT Misc-difference 63 /note= "optionally replaced with Trp"
 FT FT
 FT Misc-difference 67 /note= "optionally replaced with Asp"
 FT FT
 FT Misc-difference 69 /note= "optionally replaced with Glu"
 FT FT
 FT Misc-difference 75 /note= "optionally replaced with Pro"
 FT FT
 FT Misc-difference 82 /note= "optionally replaced with Glu or Thr"
 FT FT
 FT Misc-difference 88 /note= "optionally replaced with Pro"
 FT FT
 FT Misc-difference 94 /note= "optionally replaced with Tyr"
 FT FT
 FT Misc-difference 95 /note= "optionally replaced with Asp"
 FT FT
 FT Misc-difference 96 /note= "optionally replaced with Gln"
 FT FT
 FT Misc-difference 101 /note= "optionally replaced with Thr"
 FT FT
 FT Misc-difference 102 /note= "optionally replaced with Leu"
 FT FT
 FT Misc-difference 104 /note= "optionally replaced with Ser"
 FT FT
 FT Misc-difference 107 /note= "optionally replaced with Ser, Asp, Glu or Thr"
 FT FT
 FT Misc-difference 110 /note= "optionally replaced with Met, Thr or Glu"
 FT FT
 FT Misc-difference 114 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 115 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 126 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 132 /note= "optionally replaced with Asn"
 FT FT
 FT Misc-difference 134 /note= "optionally replaced with Thr"
 FT FT
 FT Misc-difference 162 /note= "optionally replaced with Ala"
 FT FT
 FT Misc-difference 166

FT /note= "optionally replaced with Asn"
 FT Misc-difference 169
 FT /note= "optionally replaced with Ala"
 FT Misc-difference 171
 FT /note= "optionally replaced with Asn"
 FT Misc-difference 172
 FT /note= "optionally replaced with Asn"
 FT Misc-difference 179
 FT /note= "optionally replaced with Thr"
 FT Misc-difference 183
 FT /note= "optionally replaced with Lys"
 FT Misc-difference 194
 FT /note= "optionally replaced with Asn"
 FT Misc-difference 196
 FT /note= "optionally replaced with Thr"
 FT Misc-difference 229
 FT /note= "optionally replaced with Thr"
 FT Misc-difference 225
 FT /note= "optionally replaced with Arg"
 FT Misc-difference 227
 FT /note= "optionally replaced with Glu"
 FT Misc-difference 270
 FT /note= "optionally replaced with Gly"

WO200058465-A2.

05-OCT-2000.

20-MAR-2000; 2000WO-US06417.

30-MAR-1999; 99US-0126839.

21-JUN-1999; 99US-0140077.

21-JUN-1999; 99US-0140155.

20-OCT-1999; 99US-0160566.

18-FEB-2000; 2000US-0183398.

(ELIL) LILLY & CO ELI.

Becker GW, Cohen FJ, Gonzalez-dewhitt PA, Hale JE, Micanovic R;

Newton CM, Noblitt TW, Rathmachalam R, Tschang SR, Witcher DR;

Wroblewski WJ;

WPI: 2000-656157/53.

N-PSDB; AAA75999.

FAS Ligand Inhibitory Protein analogs useful for treating abnormal

apoptosis related diseases e.g. acute lung injury, pulmonary fibrosis,

chronic obstructive pulmonary disease ulcerative colitis or Crohn's

disease

Claim 1; Page 112-113; 114pp; English.

The present sequence represents a mature human FAS Ligand Inhibitory

Protein (FLINT). FLINT is a homologue of tumour necrosis factor receptor

proteins. FLINT inhibits the binding of FAS to FAS ligand. The mature

FLINT protein is modified to produce analogues, which have greater

potency, longer in vivo half-lives, decreased aggregation, decreased

absorption onto surfaces, increased solubility and improved ease of

formulation. The FLINT analogue is useful for treating a patient

suffering from disease or condition relating to abnormal apoptosis such

as acute lung injury, acute respiratory distress syndrome, pulmonary

fibrosis, chronic obstructive pulmonary disease, ulcerative colitis, or

Crohn's disease.

XX Sequence 271 AA;
 Query Match 100.0%; Score 1491; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 VAEFTYPRDRAETGERLYCAQCPGTFVQRCRRDSPTCGPCPRHYTQFNLYLRCR 60

1 VAEFTYPRDRAETGERLYCAQCPGTFVQRCRRDSPTCGPCPRHYTQFNLYLRCR 60

QY 61 YCNVLGGERERARACHATHNRACRGTGFFAHAGFCLFHASCPGAGVIAPGPSQNTQ 120
 DB 61 YCNVLGGERERARACHATHNRACRGTGFFAHAGFCLFHASCPGAGVIAPGPSQNTQ 120
 QY 121 COPCPGTFSSASSSSSEOCOPHNCNTALGALNVPGSSSHDTCTCTGEPPLSTRVPGAE 180
 DB 121 COPCPGTFSSASSSSSEOCOPHNCNTALGALNVPGSSSHDTCTCTGEPPLSTRVPGAE 180
 QY 181 ECERAVIDFVAFODISIKRIQLRLQALEAPEGPGTTPRAGRAALQLKRLRLTLLGAQD 240
 DB 181 ECERAVIDFVAFODISIKRIQLRLQALEAPEGPGTTPRAGRAALQLKRLRLTLLGAQD 240
 QY 241 GALLVRLQALRVARMPEGLERSVREERFLPVH 271
 DB 241 GALLVRLQALRVARMPEGLERSVREERFLPVH 271

RESULT 3

AAB19705

ID AAB19705 standard; Protein; 271 AA.

XX AC AAB19705;

XX DT 05-FEB-2001 (first entry)

XX Human FAS ligand inhibitor protein FLINT.

XX FLINT; FAS ligand inhibitor protein; human; protease resistant;

XX acute lung injury; acute respiratory distress syndrome;

XX chronic obstructive pulmonary disease; pulmonary fibrosis;

XX ulcerative colitis; therapy; organ transplantation.

XX Homo sapiens.

XX Key Location/Qualifiers

XX Cleavage-site 218..219

XX /note= "cleaved by trypsin-like proteases"

XX Misc-difference 34

XX /note= "optionally replaced by Arg, as given in

XX Claims 10, 11, 13 and 14"

XX Misc-difference 36

XX /note= "optionally replaced by Thr, as given in

XX Claims 10, 11, 13 and 14"

XX Misc-difference 132

XX /note= "optionally replaced by Asn, as given in

XX Claim 12"

XX Misc-difference 194

XX /note= "optionally replaced by Asn, as given in

XX Claims 11 and 14"

XX Misc-difference 196

XX /note= "optionally replaced by Thr, as given in

XX Claims 11 and 14"

XX Misc-difference 214

XX /note= "optionally replaced by any naturally

XX occurring amino acid"

XX Misc-difference 215

XX /note= "optionally replaced by any naturally

XX occurring amino acid"

XX Misc-difference 216

XX /note= "optionally replaced by any naturally

XX occurring amino acid, preferably Pro as

XX given in Claims 9 and 15"

XX Misc-difference 217

XX /note= "optionally replaced by any naturally

XX occurring amino acid, preferably Tyr as

XX given in Claim 9"

XX Misc-difference 218

XX /note= "optionally replaced by any naturally

XX occurring amino acid, preferably Gln, Glu,

XX Ala, Gly, Ser, Val, Tyr or Asn as given in

XX Claims, 9, 10, 11, 12, especially Gln as

XX given in Claims 13, 14, 15, 35 and 36"

FT Misc-difference 213 /note= "optionally replaced by any naturally
FT occurring amino acid"
FT Misc-difference 220 /note= "optionally replaced by any naturally
FT occurring amino acid"
FT Misc-difference 221 /note= "optionally replaced by any naturally
FT occurring amino acid"
FT Misc-difference 222 /note= "optionally replaced by any naturally
FT occurring amino acid"
XX WO200058466-A2.
XX 05-OCT-2000.
XX 20-MAR-2000; 2000WO-US06418.
XX 30-MAR-1999; 99US-0126839.
XX 21-JUN-1999; 99US-0140073.
XX 04-AUG-1999; 99US-0147371.
XX 20-OCT-1999; 99US-0160524.
XX 21-OCT-1999; 99US-0160669.
XX 20-DEC-1999; 99US-0172744.
XX 26-JAN-2000; 2000US-0178134.
XX (ELIL) LILLY & CO ELI.
XX Micanovic R, Rathnachalam R, Witcher DR;
XX WPI; 2000-664925/64.
XX N-PSDB; AAP88730.
XX Novel protease resistant FAS ligand inhibitory protein analogues
FT resistant to in vivo or in vitro proteolysis at amino acid position 218
FT of the mature protein, useful for treating autoimmune diseases -
XX Claim 1; Page 94-95; 100pp; English.
XX The present sequence is that of human FAS ligand inhibitory protein
CC FLINT mature protein. FLINT is a tumour necrosis factor receptor
CC homologue that binds FAS ligand, preventing its interaction with
CC FAS. This interaction is implicated in runaway apoptosis and
CC inflammatory disease. FLINT also binds to LIGHT, a membrane-bound
CC ligand, which may play a role in immune modulation and apoptosis.
CC The invention relates to novel FLINT analogues (see also AAB19706-09)
CC that are resistant to proteolysis by trypsin-like proteases between
CC positions 218 and 219 of the FLINT mature protein sequence. The
CC analogues have amino acid substitutions in the region comprising
CC amino acids 214-222, and may contain additional substitutions at
CC residues 34, 35, 132, 194 and/or 196. Nucleic acids, vectors and
CC transformed host cells for recombinant production of the analogues
CC are claimed. FLINT cDNA (see AAA88730) is used as a template for
CC introducing the required point mutations. The protease resistant
CC FLINT analogues are used to prevent or treat acute lung injury,
CC acute respiratory stress syndrome, ulcerative colitis, chronic
CC obstructive pulmonary disease, pulmonary fibrosis, to inhibit T
CC lymphocyte activation, and to facilitate organ preservation for
CC transplantation (claimed).
XX Sequence 271 AA;
Query Match 100.0%; Score 1491; DB 21; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.3e-114;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAEPTYPWRDAETGERLVCAQCPPTGTFVORPCRDSPTTCGPPPHYTQFWNYLERCR 60
DB 1 VAEPTYPWRDAETGERLVCAQCPPTGTFVORPCRDSPTTCGPPPHYTQFWNYLERCR 60
QY 61 YCNVLGGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPPGAGVIAFGTPSQNTQ 120

Db 61 YCNVLGGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPPGAGVIAFGTPSQNTQ 120
QY 121 CQCPPTGTFSSASSSSQCOPIHNCNTALGLALNVPSSSHDTLCTSCGTGFLSTRVPGAE 180
Db 121 CQCPPTGTFSSASSSSQCOPIHNCNTALGLALNVPSSSHDTLCTSCGTGFLSTRVPGAE 180
QY 181 ECEBRAVIDFVAFOQISIKRLQRLQALEAPEGWGPTPRAGRAALQLKLRLRELTLLGAQD 240
Db 181 ECEBRAVIDFVAFOQISIKRLQRLQALEAPEGWGPTPRAGRAALQLKLRLRELTLLGAQD 240
QY 241 GALLVRLLOALRVARMPLGLERSVRERELPVH 271
Db 241 GALLVRLLOALRVARMPLGLERSVRERELPVH 271
RESULT 4
AA97247
ID AAY97247 standard; Protein; 271 AA.
XX AAY97247;
XX 19-DEC-2000 (first entry)
XX M68 TNF receptor related protein (mature protein).
XX M68; tumour necrosis factor; TNF; programmed cell death; apoptosis;
XX receptor; immune response; cell differentiation; ligand; cancer;
XX bone disease; systemic lupus erythematosus; Hashimoto's thyroiditis;
XX Grave's disease; idiopathic myxedema; autoimmune diabetes;
XX thrombotic thrombocytopenic purpura; multiple sclerosis;
XX liver diseases; autoimmune gastritis; ulcerative colitis;
XX glomerulonephritis; pulmonary fibrosis; heart failure;
XX atherosclerosis; aplastic anaemia; myelodysplastic syndromes;
XX osteoporosis; Alzheimers disease; Parkinsons disease; stroke;
XX myocardial infarction; human.
XX Homo sapiens.
XX WO200046247-A1.
XX 10-AUG-2000.
XX 04-FEB-2000; 2000WO-US03037.
XX 05-FEB-1999; 99US-0118902.
XX 20-DEC-1999; 99US-0172754.
XX (MERI) MERCK & CO INC.
XX Bai C;
XX WPI; 2000-506066/45.
XX Isolated human M68 nucleic acids and proteins which are part of the
XX tumor necrosis factor receptor (TNFR) family, useful for identifying
XX modulators that may be used to treat various diseases e.g. cancer,
XX osteoporosis, Alzheimer's disease
XX Claim 1; Page 76; 80pp; English.
XX The M68 protein is a member of a family of proteins which have
XX roles in immune responses, cell death, cell proliferation and
XX stimulation of cell differentiation. M68 lacks a transmembrane domain
XX and is a secreted factor suggesting that it functions as a natural
XX inhibitor for its ligand. The altered expression pattern of M68 in a
XX multitude of tissues suggests that M68 may play a role in cancer by
XX binding to its ligand and blocking apoptotic cell death induced by
XX such a ligand. This anti-apoptotic role of M68 suggests that
XX modulators of M68 will be useful in treatment of apoptosis-related
XX diseases such as various forms of cancer and various bone disorders.
XX M68 nucleic acids and proteins are therefore useful for treating
XX conditions involving atypical apoptosis and for identifying
XX modulators of M68. Modulators of M68 are useful for treatment of

CC cancer and other diseases associated with abnormal levels of
 CC apoptosis including systemic lupus erythematosus, Hashimoto's
 CC thyroiditis, Grave's disease, idiopathic myxedema, autoimmune
 CC diabetes, thrombotic thrombocytopenic purpura, multiple sclerosis,
 CC liver diseases, autoimmune gastritis, ulcerative colitis,
 CC glomerulonephritis, pulmonary fibrosis, heart failure,
 CC atherosclerosis, aplastic anaemia, myelodysplastic syndromes,
 CC osteoporosis, Alzheimer's disease, Parkinson's disease, stroke, and
 CC myocardial infarction.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTFWRDAETGERLVCAQCPPTGVQPCRRDSPTTCGPPRHVTQFMYLERCR 60
 DB 1 VAETPTFWRDAETGERLVCAQCPPTGVQPCRRDSPTTCGPPRHVTQFMYLERCR 60

QY 61 YCNVLGGEREEARACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120
 DB 61 YCNVLGGEREEARACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120

QY 121 CQCPPTGTFSSSSSEOCQPHNCTALGALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 DB 121 CQCPPTGTFSSSSSEOCQPHNCTALGALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180

QY 181 ECERAVIDFVAFQDISIKRLQLLQALEAPEGNGPTPRAGRAALQLKRLRLTELLGAQD 240
 DB 181 ECERAVIDFVAFQDISIKRLQLLQALEAPEGNGPTPRAGRAALQLKRLRLTELLGAQD 240

QY 241 GALLVRLLOALRVARMPLGLSVRRERFLPVH 271
 DB 241 GALLVRLLOALRVARMPLGLSVRRERFLPVH 271

RESULT 5

AA96598
 ID AA96598 standard; Protein; 271 AA.

AC AA96598;

DT 26-SEP-2000 (first entry)

XX Homo sapiens.

XX Human mature FLINT.

FLINT; osteoprotegerin 3; OPG3; tumour necrosis factor receptor; TNFR;
 FasL; LIGHT; apoptosis; pro-inflammatory; hepatotropic; vasotrophic;
 anti-diabetic; anti-anaemic; neuroprotective; anti-ulcer; cytostatic;
 anti-inflammatory; antibacterial; immunosuppressive.

OS Homo sapiens.

PN WO200337094-A2.

PD 29-JUN-2000.

PF 21-DEC-1999; 99WO-US30734.

PR 22-DEC-1998; 98US-0113407.

PR 30-MAR-1999; 99WO-US06797.

PR 20-OCT-1999; 99US-0172239.

PA (ELIL) LILLY & CO ELI.

PI Cohen FU, Posada CA, Wierda D;

DR WPI; 2000-475441/41.

DR N-PSDB; AAA51077.

XX Use of mature FLINT for treating e.g. acute respiratory distress
 XX syndrome, ulcerative colitis or ischemic injury during organ

PT transplantation

XX Example 8; Fig 3; 125pp; English.

XX Human FLINT (also known as osteoprotegerin 3) is a new tumour necrosis
 CC factor receptor (TNFR) superfamily member, which binds FasL and LIGHT and
 CC prevents FasL-Fas interaction. Mature FLINT (mFLINT) inhibits FasL-Fas
 CC mediated apoptotic and pro-inflammatory activity. mFLINT is useful for
 CC treating acute respiratory distress syndrome, treating or inhibiting
 CC ulcerative colitis, inhibiting ischemic injury during organ
 CC transplantation or for organ preservation during transplantation. mFLINT
 CC can also be used to treat acute liver failure, inflammation of the liver,
 CC abnormal (hepatocyte) apoptosis, sepsis, disorders associated with
 CC inflammation, hepatitis, ischemia, hypercoagulation or reperfusion,
 CC damage to a cardiac myocyte resulting from abnormal myocardial ischemia,
 CC Type I diabetes, cancer, damage to an innocent bystander tissue induced
 CC by a chemotherapeutic or therapeutic irradiation, aplastic anaemias,
 CC myelodysplastic syndromes and pancytopenic conditions.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 21; Length 271;

Best Local Similarity 100.0%; Pred. No. 1.3e-114;

Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTFWRDAETGERLVCAQCPPTGVQPCRRDSPTTCGPPRHVTQFMYLERCR 60

DB 1 VAETPTFWRDAETGERLVCAQCPPTGVQPCRRDSPTTCGPPRHVTQFMYLERCR 60

QY 61 YCNVLGGEREEARACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120

DB 61 YCNVLGGEREEARACHATHNRCRCRTGFFAHAGFCLEHASCPGAGVIAPGTPSQNTQ 120

QY 121 CQCPPTGTFSSSSSEOCQPHNCTALGALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180

DB 121 CQCPPTGTFSSSSSEOCQPHNCTALGALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180

QY 181 ECERAVIDFVAFQDISIKRLQLLQALEAPEGNGPTPRAGRAALQLKRLRLTELLGAQD 240

DB 181 ECERAVIDFVAFQDISIKRLQLLQALEAPEGNGPTPRAGRAALQLKRLRLTELLGAQD 240

QY 241 GALLVRLLOALRVARMPLGLSVRRERFLPVH 271

DB 241 GALLVRLLOALRVARMPLGLSVRRERFLPVH 271

RESULT 6

AA03567

ID AA03567 standard; Protein; 271 AA.

XX AA03567;

XX 04-AUG-2001 (first entry)

XX Human mature fas ligand inhibitory protein (FLINT).

Human; fas ligand inhibitory protein; FLINT; acute lung injury; ALI;
 TNFR; tumour necrosis factor receptor protein; ulcerative colitis; ARDS;
 acute respiratory distress syndrome; pulmonary fibrosis; PF; therapy;
 chronic obstructive pulmonary disease; COPD; acute lung injury; goitre;
 rheumatoid arthritis; fibroproliferative lung disease; ischaemia; sepsis;
 fibrotic lung disease; human immunodeficiency virus; HIV; osteoporosis;
 chronic renal failure; graft-vs-host disease; cutaneous inflammation;
 vascular leak syndrome; Helicobacter pylori infection; atherosclerosis;
 insulin dependent diabetes mellitus (IDDM); inflammatory bowel disease;
 Crohn's disease; pancreatitis; cancer; autoimmune disease; psoriasis;
 Down's syndrome; multiple sclerosis; cytostatic; neurotropic;
 neuroprotective; vasotrophic.

OS Homo sapiens.

XX Key Location/Qualifiers

XX Modified-site 144

XX

FT Modified-site /note= "N-linked glycosylation site"
 174
 FT Modified-site /note= "C-linked glycosylation site"
 216
 FT Modified-site /note= "O-linked glycosylation site"
 218..219
 FT Cleavage-site /note= "Proteolytic cleavage"
 XX
 XX WO200142463-A1.
 XX
 XX 14-JUN-2001.
 XX
 XX 29-NOV-2000; 2000WO-US30166.
 XX
 XX 07-DEC-1999; 99US-0169367.
 PR 07-DEC-1999; 99US-0169381.
 PR 07-DEC-1999; 99US-0169412.
 PR 23-MAR-2000; 2000US-0191430.
 XX
 XX (ELIL) LILLY & CO ELI.
 XX
 XX Lu J, Witcher DR;
 PI
 XX WPI; 2001-381684/40.
 DR N-PSDB; AAD07380.
 DR

XX New FLINT polypeptide for treating and/or preventing acute lung injury,
 PT acute respiratory distress syndrome, ulcerative colitis, and
 PT graft-versus-host disease, comprises O-linked or N-linked
 PT oligosaccharides -
 XX

Example 1; Page 52-53; 60pp; English.

XX The present sequence is human mature fas ligand inhibitory protein
 CC (FLINT). FLINT, a homologue of tumour necrosis factor receptor
 CC protein (TNFR), binds fas ligand (FasL) and thereby preventing the
 CC interaction of FasL with fas. FLINT comprising O-linked or N-linked
 CC oligosaccharides is useful for preventing or treating acute lung injury
 CC (ALI), acute respiratory distress syndrome (ARDS), ulcerative colitis,
 CC chronic obstructive pulmonary disease (COPD) and pulmonary fibrosis (PF),
 CC to facilitate organ preservation for transplantation and to inhibit T
 CC lymphocyte activation. FLINT is useful for treating and/or preventing
 CC diseases such as rheumatoid arthritis, fibroproliferative lung disease,
 CC fibrotic lung disease, acute lung injury, human immunodeficiency virus
 CC (HIV), ischaemia, brain trauma/injury, chronic renal failure, graft-vs-
 CC host disease, cutaneous inflammation, vascular leak syndrome,
 CC Helicobacter pylori infection, goitre, atherosclerosis, insulin dependent
 CC diabetes mellitus (IDDM), osteoporosis, inflammatory bowel disease,
 CC Crohn's disease, sepsis, pancreatitis, cancer, autoimmune disease such as
 CC psoriasis, Down's syndrome, and multiple sclerosis.
 XX

XX Sequence 271 AA;
 CC
 CC Query Match 100.0%; Score 1491; DB 22; Length 271;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 CC Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDPTTCGCPPRHYTQFWNYLERCR 60
 DB 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDPTTCGCPPRHYTQFWNYLERCR 60
 QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPPGAGVIAPGTPSNTQ 120
 DB 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPPGAGVIAPGTPSNTQ 120
 QY 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 DB 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 QY 181 ECERAVIDFVAFODISIKRLQRLLOALEAPEGWGPTPRAGRAALCLKRLRLTELLGAQD 240
 DB 181 ECERAVIDFVAFODISIKRLQRLLOALEAPEGWGPTPRAGRAALCLKRLRLTELLGAQD 240

QY 241 GALLIVRLLOALRVARMPGLSRSVRERFLPVH 271
 DB 241 GALLIVRLLOALRVARMPGLSRSVRERFLPVH 271

RESULT 7
 AAB68044
 ID AAB68044 standard; Protein; 271 AA.

XX AAB68044;

XX 29-JUN-2001 (first entry)

XX Amino acid sequence of a human mature FLINT polypeptide.

XX FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
 KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.

XX Homo sapiens.

XX WO200118055-A1.

XX 15-MAR-2001.

XX 31-AUG-2000; 2000WO-US20807.

XX 10-SEP-1999; 99US-0153339.

XX (ELIL) LILLY & CO ELI.

XX Atkinson PR, Tian Y, Witcher DR;

XX WPI; 2001-273382/28.

XX Compositions comprising a divalent metal cation and a FAS Ligand of
 PT Inhibitory Protein (FLINT), for reducing or inducing aggregation of
 PT FLINT and for treating diseases involving FasL/Fas and/or
 PT LIGHT/LT-beta-R receptor interactions -
 XX

XX Example 1; Page 39-40; 44pp; English.

XX The present sequence represents a mature FLINT (FAS Ligand Inhibitory
 CC Protein) polypeptide. The specification describes a composition
 CC comprising a divalent metal cation and FLINT protein. The composition
 CC is used either for reducing, reversing or eliminating aggregation and
 CC precipitation of FLINT or for inducing oligomerisation or aggregation
 CC of FLINT molecules. They can be used for purifying FLINT and/or
 CC maintaining FLINT in solution. The compositions are used to treat
 CC and/or prevent disorders associated with the binding of Fas to FasL
 CC and/or Light to the LtbetaR and/or TR2/HVEM receptors. Uses include the
 CC treatment of acute liver failure and cerebral ischemia and the prevention
 CC of apoptosis.
 XX

XX Sequence 271 AA;
 CC
 CC Query Match 100.0%; Score 1491; DB 22; Length 271;
 CC Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 CC Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDPTTCGCPPRHYTQFWNYLERCR 60
 DB 1 VAETPTVPRDAETGERLVCAQCPGTFVQPCRRDPTTCGCPPRHYTQFWNYLERCR 60
 QY 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPPGAGVIAPGTPSNTQ 120
 DB 61 YCNVLCGEREEERACHATHNRACRGTGFFAHAGFCLFHASCPPGAGVIAPGTPSNTQ 120
 QY 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 DB 121 CQCPPTGTFASSSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 QY 181 ECERAVIDFVAFODISIKRLQRLLOALEAPEGWGPTPRAGRAALCLKRLRLTELLGAQD 240

Db 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240
 Qy 241 GALLVRLQLALRVARMPLGLSVRRERFLPVH 271
 Db 241 GALLVRLQLALRVARMPLGLSVRRERFLPVH 271

RESULT 8
 AAB68047
 ID AAB68047 standard; Protein; 271 AA.
 AC AAB68047;
 DT 29-JUN-2001 (first entry)
 DE Amino acid sequence of a human mature FLINT polypeptide.
 KW FLINT; FAS ligand inhibitory protein; divalent metal cation; Fas;
 KW Fas ligand; acute liver failure; cerebral ischemia; apoptosis.
 XX Homo sapiens.
 OS
 PN WO200118041-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US20805.
 XX
 PR 10-SEP-1999; 99US-0153445.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Atkinson PR, Tian Y, Witcher DR;
 XX
 DR WPI; 2001-273381/28.
 XX
 CC Compositions comprising a divalent metal cation and a FAS Ligand
 CC Inhibitory Protein (FLINT), for reducing or inducing aggregation of
 PT FLINT and for treating diseases involving FasL/Fas and/or
 PT L-GHT/LT-beta-R receptor interactions -
 XX
 PS Disclosure; Page 30-31; 33pp; English.
 XX
 CC The present sequence represents a human mature FLINT (FAS Ligand
 CC Inhibitory Protein) polypeptide. The specification describes a
 CC composition comprising a divalent metal cation and FLINT protein. The
 CC composition is used either for reducing, reversing or eliminating
 CC aggregation and precipitation of FLINT or for inducing oligomerisation
 CC or aggregation of FLINT molecules. They can be used for purifying FLINT
 CC and/or maintaining FLINT in solution. The compositions are used to treat
 CC and/or prevent disorders associated with the binding of Fas to FasL
 CC and/or LIGHT to the Lbeta-1 and/or TR2/HVEM receptors. Uses include the
 CC treatment of acute liver failure and cerebral ischemia and the prevention
 CC of apoptosis.
 XX
 SQ Sequence 271 AA;
 Query Match 100.0%; Score 1491; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPHRYTQFWNYLRCR 60
 Db 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPHRYTQFWNYLRCR 60

Qy 61 YCNVLCGEREEARACHATHNRCRTGFFAHAGFCLFHASCPPGAGVIAPGTPSQNTQ 120
 Db 61 YCNVLCGEREEARACHATHNRCRTGFFAHAGFCLFHASCPPGAGVIAPGTPSQNTQ 120

Qy 121 COPCPPTGTSASSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 Db 121 COPCPPTGTSASSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180

Qy 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240
 Db 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240

Qy 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240
 Db 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240

Qy 241 GALLVRLQLALRVARMPLGLSVRRERFLPVH 271
 Db 241 GALLVRLQLALRVARMPLGLSVRRERFLPVH 271

RESULT 9
 AAB74465
 ID AAB74465 standard; protein; 271 AA.
 AC AAB74465;
 DT 30-MAY-2001 (first entry)
 DE Human FLINT mature protein.
 KW Human; FLINT; FAS ligand inhibitory protein; analogue; apoptosis;
 KW inflammatory disease.
 XX Homo sapiens.
 OS
 PN WO200118202-A2.
 XX
 PD 15-MAR-2001.
 XX
 PF 31-AUG-2000; 2000WO-US20806.
 XX
 PR 10-SEP-1999; 99US-0153433.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Atkinson PR, Tian Y, Witcher DR;
 XX
 DR WPI; 2001-257796/26.
 XX
 PT Compositions useful for reducing/inducing aggregation of a FLINT analog
 PT comprise a divalent metal cation and a protease-resistant FAS Ligand
 PT Inhibitory Protein (FLINT) analog -
 XX
 PS Claim 4; Page 41-42; 44pp; English.
 XX
 CC The present invention describes a composition comprising a divalent metal
 CC cation associated with a protease resistant Fas ligand inhibitory protein
 CC (FLINT) analogue. The composition is useful in the treatment of diseases
 CC associated with Fas binding to its ligand, such as acute liver failure,
 CC inflammatory diseases, cerebral ischaemia and apoptosis. The present
 CC sequence is the mature FLINT protein.
 XX
 SQ Sequence 271 AA;
 Query Match 100.0%; Score 1491; DB 22; Length 271;
 Best Local Similarity 100.0%; Pred. No. 1.3e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPHRYTQFWNYLRCR 60
 Db 1 VAETPTYPWRDAETGERLVCAQCPGTFVQPCRRDSPTTCGCPPHRYTQFWNYLRCR 60

Qy 61 YCNVLCGEREEARACHATHNRCRTGFFAHAGFCLFHASCPPGAGVIAPGTPSQNTQ 120
 Db 61 YCNVLCGEREEARACHATHNRCRTGFFAHAGFCLFHASCPPGAGVIAPGTPSQNTQ 120

Qy 121 COPCPPTGTSASSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180
 Db 121 COPCPPTGTSASSSSSQCPHNRCTALGLALNVPSSSHDTLCTCTGFPPLSTRVPGAE 180

Qy 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240
 Db 181 ECERAVIDFAFQDISIKRLQLLQALPEAGWGPTPRAGRAALQKLRRRLTELLGAQD 240

QY 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271
 DB 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271

RESULT 10
 ID AAC18767
 ID AAC18767 standard; Protein; 271 AA.
 AC AAC18767;
 XX 28-OCT-2002 (first entry)
 LT Human FLINT mature protein.
 DE Human FLINT mature protein.
 XX Human; FLINT; isoform: glycoprotein; apoptosis; sialic acid;
 KW FAS ligand inhibitory protein; autoimmune disease; inflammatory disease;
 KW infection; ischaemia; cancer; anti-inflammatory; immunomodulator;
 KW antibacterial; viricide; vasotropic; neuroprotective; nontropic;
 KW osteopathic; cytostatic; antianaemic; nephrotropic; cardiant;
 KW cardiovascular; hepatotropic.
 XX Homo sapiens.
 OS

XX Key Location/Qualifiers
 FH Modified-site 144
 FT /note= "N-linked glycosylation site"
 FT Modified-site 174
 FT /note= "O-linked glycosylation site"
 FT Modified-site 216
 FT /note= "O-linked glycosylation site"
 XX WO200260947-A2.
 XX 08-AUG-2002.
 XX 18-JAN-2002; 2002WO-US000509.
 XX 01-FEB-2001; 2003US-265690P.
 XX (ELIL) LILLY & CO ELI.
 XX Jenkins N, Witcher DR, Wroblewski VJ;
 XX WPI; 2002-627468/67.
 XX N-PSDB; AAL48978.
 XX Composition used for treating inflammatory and autoimmune diseases e.g.
 XX graft-versus-host disease, infectious diseases, ischemia and
 XX reperfusion conditions or osteoporosis comprises Fas ligand inhibitory
 XX protein analog isoform -
 XX
 PS Example 1; Page 41-42; 47pp; English.
 XX
 CC The present invention relates to a composition comprising a Fas ligand
 CC inhibitory protein (FLINT) analogue isoform. The analogue comprises a
 CC FLINT protein where a change in the sequence results in an additional
 CC glycosylation site. The composition has an average sialic acid content of
 CC 0.5-9.5 sialic acids per molecule of FLINT. The composition can be used
 CC for regulating apoptosis and for treating or preventing inflammatory and
 CC autoimmune diseases (particularly rheumatoid arthritis, inflammatory
 CC bowel disease, graft-versus-host disease, insulin-dependent diabetes,
 CC pancreatitis, psoriasis, multiple sclerosis, Grave's disease, transplant
 CC rejection, autoimmune gastritis or fibrosing lung disease), infectious
 CC diseases (particularly HIV-induced lymphopenia, fulminant viral hepatitis
 CC B/C or chronic hepatitis/cirrhosis), ischaemia and reperfusion conditions
 CC (particularly acute coronary syndrome, acute myocardial infarction,
 CC congestive heart failure, acute cerebral ischaemia/infarction or
 CC brain/spinal cord trauma), Alzheimer's disease, chronic
 CC glomerulonephritis, osteoporosis, aplastic anaemia, myelodysplasia, or
 CC chronic obstructive pulmonary disease (COPD). The composition is also
 CC useful for cytoprotection during cancer treatment or as an adjuvant to
 CC chemotherapy. The present sequence is the human FLINT mature protein.

XX Sequence 271 AA;
 XX Query Match 100.0%; Score 1491; DB 23; Length 271;
 XX Best local Similarity 100.0%; Pred. No. 1.3e-114; Indels 0; Gaps 0;
 XX Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VAETPTYPWRDAETGBRLVCAQCPGTFVQPCRRDSPTTCGPPPHRYTQFWNYLRCR 60
 DB 1 VAETPTYPWRDAETGBRLVCAQCPGTFVQPCRRDSPTTCGPPPHRYTQFWNYLRCR 60
 QY 61 YCNVLGGEREEERACHATNTRACRCRTGFAGAGFCLEHASCPCGAGVIAAGTTPSONTQ 120
 DB 61 YCNVLGGEREEERACHATNTRACRCRTGFAGAGFCLEHASCPCGAGVIAAGTTPSONTQ 120
 QY 121 CQCPPTGTFSSSSSSSQCPHNCATGALALNVPGSSSHDTLCTCTGPELSTRVPGAE 180
 DB 121 CQCPPTGTFSSSSSSSQCPHNCATGALALNVPGSSSHDTLCTCTGPELSTRVPGAE 180
 QY 181 ECERAVIDFVAQDISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRLRLTLLGAQD 240
 DB 181 ECERAVIDFVAQDISIKRLQRLQALEAPEGWGPTPRAGRAALQLKRLRLTLLGAQD 240
 QY 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271
 DB 241 GALLVRLQALRVARMPGLERSVRERFLPVH 271

RESULT 11
 ID ABB79621 standard; Protein; 271 AA.
 XX ABB79621;
 XX 21-OCT-2002 (first entry)
 XX Human Fas ligand inhibitory protein (FLINT) mature polypeptide.
 XX
 KW Fas ligand inhibitory protein; FLINT; human; apoptosis;
 KW antirheumatic; antiarthritic; immunosuppressive; antidiabetic;
 KW antibacterial; antiinflammatory; thyromimetic; antithyroid;
 KW dermatological; hepatotropic; virucide; cardiant; nontropic;
 KW neuroprotective; cytostatic.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FH Modified-site 144
 FT /note= "N-glycosylated"
 FT Modified-site 174
 FT /note= "O-glycosylated"
 FT Modified-site 216
 FT /note= "O-glycosylated"
 XX WO200260949-A2.
 XX 08-AUG-2002.
 XX 18-JAN-2002; 2002WO-US000510.
 XX 01-FEB-2001; 2001US-265749P.
 XX (ELIL) LILLY & CO ELI.
 XX Jenkins N, Witcher DR, Wroblewski VJ;
 XX WPI; 2002-599849/64.
 XX FLINT isoforms which inhibit binding of Fas to FasL receptors, useful
 XX for treating or preventing a disease associated with diseases, such as
 XX inflammatory, autoimmune, infectious, cardiovascular and CNS disorders

PS Disclosure; Page 37-38; 42pp; English.

XX The present sequence is the human Fas ligand inhibitory protein
CC (FLINT) mature polypeptide. FLINT is a glycoprotein involved in
CC regulating apoptosis. It binds Fas ligand (FasL), thereby
CC preventing the interaction of FasL with Fas. It also binds the
CC ligand LIGHT to prevent its interaction with receptor LTBR, at
CC otherwise initiating step in a second, independent apoptotic
CC pathway. The present invention provides FLINT isoforms having an
CC average sialic acid content of 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5,
CC 4.0 or greater than 4.0 per molecule of FLINT. These can be
CC obtained by recombinant production, e.g. in AV12 RGT18 cells
CC using recombinant p-smid pIG3-FLINT. The FLINT isoforms are
CC useful for treating or preventing a disease and/or condition that
CC may be associated with the binding of Fas to FasL receptors, such
CC as inflammatory/autoimmune diseases (rheumatoid arthritis,
CC inflammatory bowel disease, graft-versus-host disease, diabetes,
CC sepsis, pancreatitis, psoriasis, multiple sclerosis, Hashimoto's
CC thyroiditis, Grave's disease, transplant rejection, systemic lupus
CC erythematosus, autoimmune gastritis), infectious diseases
CC (HIV-induced lymphopenia, fulminant viral hepatitis, chronic
CC hepatitis, cirrhosis), cardiovascular disorders (acute coronary
CC syndrome, myocardial infarction, congestive heart failure,
CC atherosclerosis, cerebral ischaemia, brain/spinal cord trauma) and
CC central nervous system (CNS) disorders. They may also be used as
CC cytoprotection during cancer treatment, as an adjuvant to
CC chemotherapy, prevention of acute lung injury and adult respiratory
CC distress syndrome (ARDS). The increased sialic acid content
CC results in slower clearance time in vivo and enhanced therapeutic
CC value.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 23; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.3e-114;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGCPRHHTQFWNYLERCR 60
DB 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGCPRHHTQFWNYLERCR 60
QY 61 YCNVLCGERREARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAGTSPQNTQ 120
DB 61 YCNVLCGERREARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAGTSPQNTQ 120
QY 121 COPCPGPTFSASSSSSECOQPHRNCNTALGLALNVPSSSHDITCTSCGTFPLSTRVPGA 180
DB 121 COPCPGPTFSASSSSSECOQPHRNCNTALGLALNVPSSSHDITCTSCGTFPLSTRVPGA 180
QY 181 ECERAVIDFVAFQDISIKRLQRLQALEAPEGWGTPPRAGRAALQLKRRRLTELLGAQD 240
DB 181 ECERAVIDFVAFQDISIKRLQRLQALEAPEGWGTPPRAGRAALQLKRRRLTELLGAQD 240
QY 241 GALLVRLQLQALRVARMMPGLERSVRRFLPVH 271
DB 241 GALLVRLQLQALRVARMMPGLERSVRRFLPVH 271

RESULT 12

AAE14578
ID AAE14578 standard; Protein; 271 AA.

XX AAE14578;

XX 01-JUL-2002 (first entry)

XX Human mature FLINT protein.

XX FLINT; Fas ligand inhibitory protein; pulmonary; lung; apoptosis;
KW organ failure; liver; kidney; pancreas; inflammatory disease;
KW neutrophil; sepsis; acute respiratory distress syndrome;
KW acute lung injury; systemic inflammatory response syndrome; SIRS;
KW multiple organ dysfunction; MODS; human.

XX OS Homo sapiens.
XX WO200209668-A2.
XX 07-FEB-2002.
XX 20-JUL-2001; 2001WO-US21105.
XX 02-AUG-2000; 2000US-222476P.
XX (ELIL) LILLY & CO ELI.
XX Micanovic R, Witcher DR;
XX WPI; 2002-206149/26.
XX N-PSDB; AAD27868.
XX Administering FLINT (Fas ligand inhibitory protein) or FLINT analog,
XX useful for treating e.g. sepsis or respiratory distress syndrome,
XX involves pulmonary administration of a therapeutic amount of the FLINT
XX or FLINT analog -
XX Disclosure; Page 29-30; 35pp; English.

XX The invention relates to a new method of administering FLINT
XX (Fas ligand inhibitory protein) or FLINT analog that involves pulmonary
XX administration of a therapeutic amount of the FLINT or FLINT analog.
XX The method enables systemic absorption of FLINT through lungs and
XX significantly reduces or eliminates the need for administering FLINT by
XX injection or other routes of administration. The method is useful in
XX treating disorders related to enhanced apoptosis (e.g. organ failure
XX in liver, kidneys and pancreas) and inflammatory diseases associated with
XX neutrophil activation (e.g. sepsis, acute respiratory distress syndrome,
XX acute lung injury, systemic inflammatory response syndrome (SIRS) and
XX multiple organ dysfunction (MODS)). The method minimises the pain
XX and discomfort of injection methods. The present sequence is human
XX mature FLINT protein.

XX Sequence 271 AA;

Query Match 100.0%; Score 1491; DB 23; Length 271;
Best Local Similarity 100.0%; Pred. No. 1.3e-114;
Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGCPRHHTQFWNYLERCR 60
DB 1 VAETPTYPWRDAETGERLVCAQCPGTFVQRCRRDSPTTCGCPRHHTQFWNYLERCR 60
QY 61 YCNVLCGERREARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAGTSPQNTQ 120
DB 61 YCNVLCGERREARACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAGTSPQNTQ 120
QY 121 COPCPGPTFSASSSSSECOQPHRNCNTALGLALNVPSSSHDITCTSCGTFPLSTRVPGA 180
DB 121 COPCPGPTFSASSSSSECOQPHRNCNTALGLALNVPSSSHDITCTSCGTFPLSTRVPGA 180
QY 181 ECERAVIDFVAFQDISIKRLQRLQALEAPEGWGTPPRAGRAALQLKRRRLTELLGAQD 240
DB 181 ECERAVIDFVAFQDISIKRLQRLQALEAPEGWGTPPRAGRAALQLKRRRLTELLGAQD 240
QY 241 GALLVRLQLQALRVARMMPGLERSVRRFLPVH 271
DB 241 GALLVRLQLQALRVARMMPGLERSVRRFLPVH 271

RESULT 13

AAW66102
ID AAW66102 standard; Protein; 300 AA.

XX AAW66102;

XX 02-DEC-1998 (first entry)

XX Amino acid sequence of tumour necrosis related receptor (TR4).

DE Human; tumour necrosis related receptor; TR4; agonist; antagonist;
 KW inhibition; chronic; acute; inflammation; arthritis; septicemia;
 KW autoimmune disease; transplant rejection; stroke; cancer;
 KW Alzheimer's disease.

XX Homo sapiens.

XX SP86:850-A1.

XX C2-SEP-1398.

XX 20-JAN-1998; 98EP-0300382.

XX C4-FEB-1997; 97US-0794796.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX Emery J, Tan KB, Truneh A, Young PR;

XX WPI; 1998-508248/44.

XX N-PSDB; AAV07654.

XX New DNA encoding tumour necrosis related receptor - used to treat
 PT and prevent e.g. inflammation, arthritis, septicemia, autoimmune
 PT diseases, transplant rejection, infection, stroke, ischaemia, ARDS,
 PT restenosis, AIDS, bone disorders and cancer

XX Claim 1; Fig 1; 2lpp; English.

XX This is the amino acid sequence of the human tumour necrosis related
 CC receptor (TR4), used in the method of the invention. The TR4 protein
 CC or its agonist can be used to treat a subject in need of enhanced
 CC TR4 polypeptide activity. The antagonist is used to inhibit TR4
 CC polypeptide activity. The active agents can be used for the
 CC treatment and prevention of diseases such as chronic and acute
 CC inflammation, arthritis, septicemia, autoimmune diseases, transplant
 CC rejection, stroke, cancer, Alzheimer's disease.

SQ Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 19; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.4e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTVMDAETGERLVCAQCPCPGTFVQPCRRDPTTCGPPRRHYTQFWNYLRCR 60
 Db 30 VAETPTVMDAETGERLVCAQCPCPGTFVQPCRRDPTTCGPPRRHYTQFWNYLRCR 89

Qy 61 YCNVLCGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTPSONTQ 120
 Db 90 YCNVLCGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTPSONTQ 149

Qy 121 CQCPPTGTFSSASSSSSQCPHNRNCTALGLALNVPGSSSHDTLCTCTGFPFLSTRVPGA 180
 Db 150 CQCPPTGTFSSASSSSSQCPHNRNCTALGLALNVPGSSSHDTLCTCTGFPFLSTRVPGA 209

Qy 181 ECEAVDVFVAFQDISIKRLQRLQALEAPGSGWGTFRAGRAALQKLRRRLTELLGAQD 240
 Db 210 ECEAVDVFVAFQDISIKRLQRLQALEAPGSGWGTFRAGRAALQKLRRRLTELLGAQD 269

Qy 241 GALLVRLQLARVARMPEGLERSVREFLFVH 271
 Db 270 GALLVRLQLARVARMPEGLERSVREFLFVH 300

RESULT 14
 AAW63622
 ID AAW63622 standard; Protein; 300 AA.
 XX
 AC AAW63622;

XX 26-OCT-1998 (first entry)

XX Human tumour necrosis factor receptor-6 alpha protein.

XX Human tumour necrosis factor receptor-6 alpha; TNFR-6 alpha; TNFR-6 beta;
 KW endothelial cells; keratinocytes; normal prostate; apoptosis;
 KW prostate tumour tissue.

XX Homo sapiens.

XX Key Location/Qualifiers
 FT Peptide 1..30
 FT Peptide 31..300
 FT /note= "TNFR-6 alpha"
 FT Region 31..282
 FT /note= "Soluble extracellular domain"

XX MO9830694-A2.

XX 16-JUL-1998.

XX 13-JAN-1998; 98WO-US06153.

XX 14-JAN-1997; 97US-0035496.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Ebner R, Feng P, Gentz RL, Ni J, Ruben SM, Yu G;

XX WPI; 1998-399142/34.

XX N-PSDB; AAV39085.

XX Human tumour necrosis factor receptors 6-alpha and 6-beta - used in
 PT the diagnosis of immune system-related disorder(s)

XX Claim 20; Fig 1; 3lpp; English.

XX The present sequence represents the human tumour necrosis factor
 CC receptor-6 alpha (TNFR-6 alpha) protein. The invention also provides
 CC for the TNFR-6 beta protein (AAW63623). TNFR-6 alpha and TNFR-6 beta
 CC are members of the tumour necrosis factor receptor (TNFR) family. TNFRs
 CC are expressed in endothelial cells, keratinocytes, normal prostate and
 CC prostate tumour tissue. For a number of disorders of these cells,
 CC particularly of the immune system, substantially altered (whether
 CC increased or decreased) levels of TNFR-6 alpha and/or TNFR-6 beta gene
 CC expression can be detected, therefore the TNFR-6 alpha and TNFR-6 beta
 CC polypeptides, nucleic acids and antibodies are claimed to be useful in
 CC the diagnosis of such disorders. Mutations of the TNFR-6 alpha and
 CC TNFR-6 beta genes can also be detected. The TNFR polypeptides are
 CC also claimed to be useful for identifying ligands which may be useful
 CC in the treatment of apoptosis related disorders.

XX Sequence 300 AA;

Query Match 100.0%; Score 1491; DB 19; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.4e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VAETPTVMDAETGERLVCAQCPCPGTFVQPCRRDPTTCGPPRRHYTQFWNYLRCR 60
 Db 30 VAETPTVMDAETGERLVCAQCPCPGTFVQPCRRDPTTCGPPRRHYTQFWNYLRCR 89

Qy 61 YCNVLCGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTPSONTQ 120
 Db 90 YCNVLCGEREEERACHATHNRCRCRTGFFAHAGFCLEHASCPCPGAGVIAPGTPSONTQ 149

Qy 121 CQCPPTGTFSSASSSSSQCPHNRNCTALGLALNVPGSSSHDTLCTCTGFPFLSTRVPGA 180
 Db 150 CQCPPTGTFSSASSSSSQCPHNRNCTALGLALNVPGSSSHDTLCTCTGFPFLSTRVPGA 209

Qy 181 ECEAVDVFVAFQDISIKRLQRLQALEAPGSGWGTFRAGRAALQKLRRRLTELLGAQD 240

Db 210 ECERAVIDFVAFQDISIXLQRLLOALEPGEWGPTFRAGRAALQKLRRRLTELLGAQD 269
 QY 241 GALLVRLQLQALVARMPGLERSVRERFLPVH 271
 Db 270 GALLVRLQLQALVARMPGLERSVRERFLPVH 300

RESULT 15

AA03099

ID AAY03099 standard; Protein; 300 AA.

XX AC

XX AAY03099;

DT 09-DEC-1999 (first entry)

DE Human lung TNF-receptor protein.

XX Tumour necrosis factor; TNF; TNF receptor; human; lung; gene therapy;
 KW detection; immunoassay; diagnosis; disease; immune system; tumour; asthma;
 KW osteogenic system; cardiovascular system; central nervous system; asthma;
 KW peripheral nervous systems; transplant incompatibility; antitumor;
 KW rheumatoid arthritis; antiasthmatic; antiarthritic.

XX Homo sapiens.

FH Key Location/Qualifiers

FT CDS 134..1036

FT /*tag= a

FT /product= "TNF-receptor"

FN DE19809978-A1.

PD 16-SEP-1993.

XX 09-MAR-1998; 98DE-1009978.

XX 09-MAR-1998; 98DE-1009978.

XX (BADI) BASF AG.

XX Kroeger B; .

XX WPI; 1999-519473/44.

XX N-PSDB; AAZ09998.

XX New soluble member of tumor necrosis factor receptor family, useful for
 XX identification specific modulators and for treating disease e.g. tumors

PS Claim 1; Page 8-9; 10pp; German.

XX This invention describes a novel tumour necrosis factor (TNF) receptor
 CC (I) isolated from human lung tissue. (I) is used: (i) to raise specific
 CC antibodies (Ab); (ii) to screen for specific (ant)agonists or ligands
 CC (A), potential therapeutic agents; and (iii) therapeutically (optionally
 CC expressed from a gene therapy vector) in conditions associated with a
 CC deficit of (I). Ab are used: (a) for qualitative or quantitative
 CC detection of (I) in standard immunoassays (for diagnosis of disease, or
 CC susceptibility, or for monitoring); and (b) as therapeutic inhibitors in
 CC cases where (I) is overexpressed. Nucleic acid (II) that encodes (I) is
 CC used: (A) for recombinant production and/or amplification assays; (C) as
 CC fragments, in standard hybridization and/or oligonucleotide
 CC source of antisense molecules or ribozymes; and (D) to produce transgenic
 CC animals (for studying (patho)physiology of (I)). Diseases possibly
 CC associated with under- or over-expression of (I) are those of the immune,
 CC osteogenic, cardiovascular and central or peripheral nervous systems,
 CC tumors, transplant incompatibility, asthma and rheumatoid arthritis. The
 CC products of the invention have antitumor, antiasthmatic and
 CC antiarthritic activity. This sequence represents the TNF-receptor of the
 XX invention.

SQ Sequence 300 AA;

Query Match. 100.0%; Score 1491; DB 20; Length 300;
 Best Local Similarity 100.0%; Pred. No. 1.4e-114;
 Matches 271; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VAETPTYPRDAETGERLVCAQCPCGTFFVQRCRDSPTTCGCPPRHYTQFWNYLERCR 60
 Db 30 VAETPTYPRDAETGERLVCAQCPCGTFFVQRCRDSPTTCGCPPRHYTQFWNYLERCR 89

QY 61 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSNTQ 120
 Db 90 YCNVLCGEREEERACHATHNRACRCRTGFFAHAGFCLEHASCPPGAGVIAPGTPSNTQ 149

QY 121 COPCPPTFSASSSSSEQCPHNCNTALGLALNVPSSSHDTICTCTGPPPLSTRVPGA 180
 Db 150 COPCPPTFSASSSSSEQCPHNCNTALGLALNVPSSSHDTICTCTGPPPLSTRVPGA 209

QY 181 ECERAVIDFVAFQDISIXLQRLLOALEPGEWGPTFRAGRAALQKLRRRLTELLGAQD 240
 Db 210 ECERAVIDFVAFQDISIXLQRLLOALEPGEWGPTFRAGRAALQKLRRRLTELLGAQD 269

QY 241 GALLVRLQLQALVARMPGLERSVRERFLPVH 271
 Db 270 GALLVRLQLQALVARMPGLERSVRERFLPVH 300

Search completed: December 3, 2003, 13:12:41
 Job time : 42 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2003, 13:11:11 ; Search time 20 Seconds
(without alignments)
1303.086 Million cell updates/sec

Title: US-10-069-385-1
Perfect score: 1491
Sequence: 1 VAEPTYPWRDAETGRLVC.....RVARMEGLRSVRFPLPVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 76:.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	340.5	22.8	461	1	A35356	tumor necrosis fac
2	333.5	22.4	459	2	I48854	gene murine tumour
3	332.5	22.3	474	2	B38634	tumor necrosis fac
4	299.5	20.1	435	2	I54182	tumor necrosis fac
5	289	19.4	651	2	JC7705	death receptor-6 -
6	260	17.4	348	2	T28623	hypothetical prote
7	260	17.4	349	2	D72175	G2R protein - vari
8	260	17.4	349	2	D36858	gene G4R protein -
9	234.5	15.7	325	2	B43692	OX40 homolog - hum
10	215.5	14.5	277	2	I37552	T2 protein - rabbi
11	211.5	14.2	271	2	S12783	OX40 antigen precu
12	211	14.2	277	2	A00771	B-cell activation
13	210.5	14.1	326	1	GQVZML	T2 protein - myxom
14	203	13.6	305	2	A46476	B cell-associated
15	194.5	13.0	272	2	I48700	gene ox40 protein
16	185	12.4	256	2	B32393	T-cell antigen 4-1
17	182	12.2	595	2	A42086	CD30 antigen precu
18	174	11.7	255	2	I18426	-lymphocyte activat
19	171.5	11.5	416	1	JN0006	nerve growth facto
20	168	11.3	425	1	A26431	nerve growth facto
21	158	10.6	427	1	GQHUN	nerve growth facto
22	155.5	10.4	327	2	A46484	apoptosis-mediati
23	148.5	10.0	1574	2	T13954	MEGF6 protein - ra
24	148	9.9	250	1	A49053	CD27 antigen precu
25	147.5	9.9	5376	2	T42215	zonadhesin - mouse
26	146.5	9.8	260	1	A46517	CD27 antigen precu
27	145	9.7	335	2	A40036	apoptosis-mediati
28	143	9.6	1620	2	T27283	hypothetical prote
29	140	9.4	314	2	I37383	FAS soluble protei

30 137.5 9.2 324 2 JC2395 Fas antigen precu

31 135.5 9.1 1299 2 T43251 furin (EC 3.4.21.7

32 135 9.1 2321 2 S78549 notch3 protein - h

33 130.5 8.8 454 1 GOMST1 tumor necrosis fac

34 128.5 8.6 3635 2 T10033 laminin alpha 5 ch

35 127 8.5 1192 2 S69000 laminin gamma 2 ch

36 125.5 8.4 1548 2 S34583 serine proteinase

37 124.5 8.4 1713 2 A55347 adhesive ligand ep

38 123.5 8.3 455 1 GQHUT1 tumor necrosis fac

39 123.5 8.3 493 2 JC5486 membrane glycoprot

40 122.5 8.2 2824 2 T22759 hypothetical prote

41 121 8.1 3106 1 S53868 laminin alpha-2 ch

42 120 8.0 1609 1 MMHUB2 laminin gamma-1 ch

43 119.5 8.0 3084 1 MMMSA laminin alpha-1 ch

44 118.5 7.9 461 1 GQRTT1 tumor necrosis fac

45 118.5 7.9 1680 2 A43434 furin (EC 3.4.21.7

ALIGNMENTS

RESULT 1

A35356

tumor necrosis factor receptor 2 precursor [validated] - human

N;Alternate names: 75K tumor necrosis factor receptor; TNF receptor type 2

C;Species: Homo sapiens (man)

C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 08-Dec-2000

C;Accession: A35356; #36475; A48416; A36007; A23666; B35010; I38094

R;Smith, C.A.; Davis, T.; Anderson, D.; Solam, L.; Beckmann, M.P.; Jerzy, R.; Dower, S.K

Science 248, 1019-1023, 1990

A;Title: A receptor for tumor necrosis factor defines an unusual family of cellular and

A;Reference number: A35356; MUID:90260639; PMID:2160731

A;Accession: A35356

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-461 <SMI>

A;Cross-references: GB:M32315; NID:gi89185; PIDN:AA53929.1; PID:gi89186

R;Kohn, T.; Brewer, M.T.; Baker, S.L.; Schwartz, P.E.; King, M.W.; Hale, K.K.; Squires,

Proc. Natl. Acad. Sci. U.S.A. 87, 8331-8335, 1990

A;Title: A second tumor necrosis factor receptor gene product can shed a naturally occur

A;Reference number: A36475; MUID:91045931; PMID:2172983

A;Accession: A36475

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 1-195, 'R', 197-461 <KOH>

A;Cross-references: GB:M55994; GB:M38549; NID:g333757; PIDN:AAA36755.1; PID:g339758

R;Dembic, Z.; Loetscher, H.; Gubler, U.; Pan, Y.C.; Lahm, H.W.; Gentz, R.; Brockhaus, M.

Cytokine 2, 231-237, 1990

A;Title: Two human TNF receptors have similar extracellular, but distinct intracellular,

A;Reference number: A48416; MUID:91370690; PMID:1966549

A;Accession: A48416

A;Status: preliminary

A;Molecule type: mRNA; protein

A;Residues: 23-461 <DEM>

A;Cross-references: GB:S63368; NID:g235648; PIDN:AAB19824.1; PID:g235649

A;Note: sequence extracted from NCBI backbone (NCBIN:63368, NCBI:P:63371)

R;Heller, R.A.; Song, K.; Onasch, M.A.; Fischer, W.H.; Chang, D.; Ringold, G.M.

Proc. Natl. Acad. Sci. U.S.A. 87, 6151-6155, 1990

A;Title: Complementary DNA cloning of a receptor for tumor necrosis factor and demonstra

A;Reference number: A36007; MUID:90349572; PMID:2166946

A;Accession: A36007

A;Status: preliminary

A;Molecule type: mRNA

A;Residues: 116-140, 'P', 142-195, 'R', 197-362, 'T', 364-461 <HEL>

A;Cross-references: GB:M58587; NID:g339751; PIDN:AA63262.1; PID:g339752

R;Loetscher, H.; Schlaeger, E.J.; Lahm, H.W.; Pan, Y.C.E.; Lesslauer, W.; Brockhaus, M.

J. Biol. Chem. 265, 20131-20138, 1990

A;Title: Purification and partial amino acid sequence analysis of two distinct tumor nec

A;Reference number: A23666; MUID:91056048; PMID:2173696

A;Accession: A23666

A;Status: preliminary

A;Molecule type: protein

A;Residues: 23-40;65-69;136-141;300-306 <LOE>

R;Engelmann, H.; Novick, D.; Wallach, D.
 J. Biol. Chem. 265, 1531-1536, 1990
 A:Title: Two tumor necrosis factor-binding proteins purified from human urine. Evidence
 A:Reference number: A35010; MUID:90110215; PMID:2153136
 A:Accession: B35010
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 27-31 <ENG>
 R;Kubert, P.; Kemper, O.; Wallach, D.
 Gene 150, 381-386, 1994
 A:Title: Cloning, sequencing and partial functional characterization of the 5' region of
 A:Reference number: 138094; MUID:95121334; PMID:7821811
 A:Accession: I38094
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-37 <RES>
 A:Cross-references: EMBL:X80021; NID:9666044; PIDN:CAA56324.1; PID:g825701
 C:Genetics:
 A:Gene: GDB:TNFR2
 A:Cross-references: GDB:125914; OMIM:131191
 A:Map position: p36.2-1p36.2
 A:Introns: 26/3
 A>Note: the list of introns is incomplete
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 C:Keywords: duplication; glycoprotein; receptor; transmembrane protein
 F:1-22/Domain: signal sequence #status predicted <SIG>
 F:23-416/Product: tumor necrosis factor receptor 2 #status experimental <MAT>
 F:40-76/Domain: NGF receptor repeat homology <NG1>
 F:78-119/Domain: NGF receptor repeat homology <NG2>
 F:120-162/Domain: NGF receptor repeat homology <NG3>
 F:164-201/Domain: NGF receptor repeat homology <NG4>
 F:262-279/Domain: transmembrane #status predicted <TMN>
 F:280-461/Domain: intracellular #status predicted <INT>
 F:171,193/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 22.8%; Score 340.5; DB 1; Length 461;
 Best Local Similarity 29.7%; Pred. No. 2e-18;
 Matches 89; Conservative 43; Mismatches 15; Indels 53; Gaps 11;

QY 1 VAETPTYPWRDAETG-----RLVCAQCPGPTFVORPCRRSDPTTCGCPPRH 48
 DB 27 VAFTPYAP-----EPGSTCLREYDQTAQMCCKSPGQHAQVFTKTSDTVDCSDST 82

QY 49 YTFQWNLRCRYCNVLGCEEEARACHATHNACRCKTGFFAHAG-----FCLHAS 102
 DB 83 YTQLNWNWPECLSGSRSSQVQVQATREGRNLCCTCPGWCHLSKQEGRLCAPLRK 142

QY 103 CPPGAGVIAPTPGQNTQCPPTGTFSSSSSECCQPHRNCITAGLALNVPSSSHDT 162
 DB 143 CRPGFGVAPGPTSDVVCPCAPGTFSTNTSTSDICRPHQCNVVA---IPGNASMDA 198

QY 163 LCTSGTGFPLSTRVPGAECEERAVIDFVAFQDISIKRLQRLQALAEPE-----GWGPTP 217
 DB 199 VCTSTS---PTSMAPGAVHLPQV-----STRSQTPTEPSTAPSTSFLLFMGSP 249

QY 218 RA-----GRAALQLKRLRLTELLGAQDGLALLVLLQAL---RVARMP-GLRSYVRRLP 269
 DB 250 PAEGSTGDFALPVGLIVGVTL-----GLLIIGVNVVNTQVKKKPLCQREAKVPHLP 304

RESULT 2
 148854
 gene murine tumour necrosis factor receptor 2 protein - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 23-Jul-1999
 C:Keywords: cytokine receptor; transmembrane protein
 C:Accession: I48854
 R;Powell, B.E.; Wicker, L.S.; Peterson, L.B.; Todd, J.A.
 Mamm. Genome 5, 726-727, 1994
 A:Title: Allelic variation of the type 2 tumor necrosis factor receptor gene.
 A:Reference number: 148854; MUID:95178848; PMID:7873884
 A:Accession: I48854
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA

A:Residues: 1-459 <RES>

A:Cross-references: EMBL:X76401; NID:9433830; PIDN:CAA53981.1; PID:g433831
 C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology
 F:151-188/Domain: NGF receptor repeat homology <NGF>

Query Match 22.4%; Score 333.5; DB 2; Length 459;

Best Local Similarity 29.7%; Pred. No. 6.8e-18;
 Matches 91; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 17 RLVCACQCPGTFVORPCRRSDPTTCGCPPRHYTVFNYLRCRYCNVLGCEEEARAC 76

DB 37 QWCCAKCPGQVYKFCNKNTSDTVACDCASMYTQWVQFRICLSCSSCSTQVETRAC 96

QY 77 HATHNACRCRTGFF-----AHAGF---CLEHACPPGAGVIAPGTPSQNTQCCPCPGTF 129

DB 97 TKQQRNVCAACEAGRYCALKTHSGCRQCMRLSKCGFGVGSRAFGNVLCACAPGTF 156

QY 130 SASSSSSECCQPHRNCITAGLALNVPSSSHDTLCT---SCTGFPLSTRVPGAEBCERA 185

DB 157 SDTTSSTDVCRPHRICSLA---IPGNASTDAVCAPESTFLSAIPRTLYVSQPEPTRSQ 212

QY 186 VIDFVAFQDISIKRLQRLQALAEPEGWGPTP-----RAGRAALQLKRLRLTELLGAQD 240

DB 213 PLD---QEPGSPQPSILTSL-----GSTPIEQSTKGISLPIGLIVGVTSL----- 257

QY 241 GALLVRLQAL-----RVARMPGLERSVRRFLP 269

DB 258 GLLMGLVNCFTLVQRKKKPSCLORDAKYPHP 290

RESULT 3

B38634

tumor necrosis factor receptor type 2 precursor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 23-Jul-1999

A:Accession: B38634; A40254; S54816

R;Lewis, M.; Tartaglia, L.A.; Lee, A.; Bennett, G.L.; Rice, G.C.; Wong, G.H.W.; Chen, E

Proc. Natl. Acad. Sci. U.S.A. 88, 2830-2834, 1991

A:Title: Cloning and expression of cDNAs for two distinct murine tumor necrosis factor

A:Reference number: A38634; MUID:91187885; PMID:1849278

A:Accession: B38634

A:Molecule type: mRNA

A:Residues: 1-474 <LEW>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R;Goodwin, R.G.; Anderson, D.; Jerzy, R.; Davis, T.; Brannan, C.I.; Copeland, N.G.; Jenl

Mol. Cell. Biol. 11, 3020-3026, 1991

A:Title: Molecular cloning and expression of the type 1 and type 2 murine receptors for

A:Reference number: A40254; MUID:91246168; PMID:1645445

A:Accession: A40254

A:Molecule type: mRNA

A:Residues: 1-474 <GOO>

A:Cross-references: GB:M60469; NID:g199827; PIDN:AAA39752.1; PID:g199828

R;Kisomergis, M.; Fellows, R.; Feldmann, M.; Chetnafovsky, Y.

submitted to the EMBL Data Library, May 1995

A:Description: Characterization of the promoter region of the murine p75-TNF receptor.

A:Reference number: S54816

A:Accession: S54816

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-22 <KIS>

A:Cross-references: EMBL:X87128; NID:g809043; PIDN:CAA60613.1; PID:g809044

C:Superfamily: tumor necrosis factor receptor type 2; NGF receptor repeat homology

C:Keywords: cytokine receptor; transmembrane protein

F:1-22/Domain: signal sequence #status predicted <SIG>

F:23-474/Product: tumor necrosis factor receptor type 2 #status predicted <MAT>

F:40-77/Domain: NGF receptor repeat homology <NG1>

F:79-120/Domain: NGF receptor repeat homology <NG2>

F:166-203/Domain: NGF receptor repeat homology <NG4>

Query Match 22.3%; Score 332.5; DB 2; Length 474;

Best Local Similarity 29.7%; Pred. No. 8.4e-18;

Matches 91; Conservative 44; Mismatches 109; Indels 39; Gaps 9;

A;Accession: JC7705
A:Molecule type: mRNA
A;Residues: 1-651 <BRI>
C;Cross-references: GB:AF349908
C;Comment: This receptor, a member of the tumor necrosis factor receptor family, belongs toresia, activates a cell death and/or survival signaling cascade.
C;Genetics:
A;Gene: dr-6
C;Keywords: signal sequence #status predicted <SIG>
P;1-21/Domain: extracellular cysteine-rich, ligand-binding #status predicted <ECL>
F;52-196/Domain: transmembrane #status predicted <TM>
F;332-350/Domain: death domain #status predicted <DED>
F;410-475/Domain: conserved cytoplasmic #status predicted

Query Match 19.4%; Score 289; DB 2; Length 651;
Best Local Similarity 33.5%; Pred.No.2.2e+14;
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

Qy 11 DAETGERLVCAQCPTGTFVQRCDSDFTTCGPPRRHYTQFWNYLRCRYCNVLCSRE 70
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq DRATNOELICDKCPAGTVKSHCTKTSLRECSPCDGTFTKHENGIERCHPCPKCELP 102
Qy 71 EEARACHATHNRACRRTGFFAHAGECLEHASCPPGAGVIAPGPSQNTQQCPPTGFS 130
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq IEKTHCTALTDRECTLSGGTFQINDTCVPYTCPVGWGVKKGTETEDVRCKPLRGTS 162
Qy 131 ASSSSSQOCQHNRCTALGLNLNPGSSHDTLCSTCGFP 171
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq DVPSSVMVKCKTYTCFGKNMNVVKETESDNVCASPSILP 203

RESULT 6
T28623
hypothetical protein G2R - variola major virus
C;Species: variola major virus
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 21-Jul-2000
C;Accession: T28623
R;Massung, R.F.; Esposito, J.J.; Liu, L.I.; Qi, J.; Utterback, T.R.; Knight, J.C.; Aubin Nature 366, 748-751, 1993
A;Title: Potential virulence determinants in terminal regions of variola smallpox virus
A;Reference number: 220488; PMID:94088747; EMBL:D264798
A;Accession: T28623
A;Status: preliminary; translated from GB/EMBL/DDBC
A:Molecule type: DNA
A;Residues: 1-348 <MAS>
A;Cross-references: EMBL:L22579; NID:g623595; PIDN:AAA60933.1; PID:g439102
A;Experimental source: strain Bangladesh 1975
C;Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 348;
Best Local Similarity 32.2%; Pred.No.1.9e-12;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

Qy 5 PTPWRDAB-TGERLVCAQCPTGTFVQRPCCRDSPTTCGPDPRHYYTQFWNYLERCRYCN 63
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq PNGKCOTEXKRHLCCLSCPGTVASRLCDSKTNQTCTPCSGGTFTSRNHLPACLSCN 86
Qy 64 VLCSERESEARACHATHNRACRRTGFF-----AHAGFCLEHASCPPGAGVIAPGPSQ 117
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq GRNSNQVETRSCNTNNRICESPFGYLKLGSSGCKACVSQTKGIGYG-V-SGHTSVG 145
Qy 118 NTQCQCPPTGFSASSSSECOQHNRCTALGLNLNPGSSHDTLCSTCGFPLSTRVP 177
Db :|||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Dq DVICSPCGFGTIYSVTSSADKEPVNNITFNVIDEITLYPNVDITSCTRTTTTLGSSEL 205
Qy 178 GAE 180
Db :::::
Dq 206 TSE 208

RESULT 7
D72175

G2R protein - variola minor virus (strain Garcia-1966)
 C:Species: variola minor virus
 C:Date: 24-Nov-1999 #sequence_revision 24-Nov-1999 #text_change 20-Jun-2000
 C:Accession: D72175
 R:Shchelkunov, S.N.; Torrenin, A.V.; Gutorov, V.V.; Saifonov, P.F.; Maseung, R.F.; Lopan
 submitted to GenBank, March 1998
 A:Description: Analysis of the complete coding sequence of DNA of alastrim variola minor
 A:Reference number: A72150
 A:Accession: D72175
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <SHC>
 A:Cross-references: GB:Y16780; NID:G5830555; PIDN:CAB54798.1; PID:G5830759
 A:Experimental source: strain Garcia-1966
 C:Genetics:
 A:Gene: G2R
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology

Query Match 17.4%; Score 260; DB 2; Length 349;
 Best Local Similarity 32.2%; Pred. No. 1.9e-12;
 Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYWRDAE-TGERLVCAQCPCPGTFVQPCRDSPPTTCGCPPRHYTOFWNYLRCRYCN 63
 DB 28 PNGCKKQTEYKRNLCCLSCPPGYASRLCDSKNTQCTPGSGTFTSRNNHLPACLSCN 87

QY 64 VLGEREEERACHATHNRCRCRTGFF-----AHAGFCLEHASCPCPGAGVIAPGTPSQ 117
 DB 88 GRCSNQVETRSCNTHNRICECSFGYYCLLKSGSGCKACVSTQKCGIGYGV-SGHTSVG 146

QY 118 NTQCPCPPGTFSSSSSSSQOQPHRNCATGLALNVPSSSHDTLCTSGTGFPLSTRVP 177
 DB 147 DVICSPCGFGYSHTVSSADKCEPVNNTFNVIDEITLYPVNMTSCTRTTTTGLSESL 206

QY 178 GAE 180
 DB 207 TSE 209

RESULT 8
 D36858
 Gene G4R protein - variola virus
 N:Alternate names: B28R protein (COP)
 C:Species: variola virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 23-Mar-2002
 C:Accession: D36858; S46888; S32385; S35987
 R:Blinov, V.M.
 submitted to GenBank, November 1992
 A:Reference number: A36859
 A:Accession: D36858
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <BLT>
 A:Cross-references: GB:X69198; NID:G456759; PIDN:CAA49137.1; PID:G457087
 A:Experimental source: strain India-1967, ssp. major, isolate Ind3
 R:Kolykhalov, A.A.; Blinov, V.M.; Gutorov, V.V.; Podnyakov, S.G.; Chizhikov, V.E.; Prok
 submitted to the EMBL Data Library, April 1992
 A:Description: Nucleotide sequence analysis of the region of Variola virus XhoI F O H P
 A:Reference number: S46888
 A:Accession: S46888
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-349 <KOL>
 A:Cross-references: EMBL:X67117; NID:G516428; PIDN:CAA47540.1; PID:G516449
 A:Experimental source: strain India-1967, isolate Ind3
 R:Shchelkunov, S.N.; Blinov, V.M.; Sandakhtchiev, L.S.
 FEBS Lett. 319, 80-83, 1993
 A:Title: Genes of variola and vaccinia viruses necessary to overcome the host protective
 A:Reference number: S32385; MUID:93202281; PMID:8384129
 A:Accession: S32385
 A:Molecule type: DNA
 A:Residues: 31-168 <SHC>
 A:Cross-references: EMBL:X69198

A:Experimental source: strain India-1967, ssp. major
 C:Genetics:
 A:Gene: G4R
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 P:32-66/Domain: NGF receptor repeat homology <NG3>
 P:68-109/Domain: NGF receptor repeat homology <NG2>
 P:110-151/Domain: NGF receptor repeat homology <NG3>

Query Match 17.4%; Score 260; DB 2; Length 349;
 Best Local Similarity 32.2%; Pred. No. 1.9e-12;
 Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;

QY 5 PTYWRDAE-TGERLVCAQCPCPGTFVQPCRDSPPTTCGCPPRHYTOFWNYLRCRYCN 63
 DB 28 PNGCKKQTEYKRNLCCLSCPPGYASRLCDSKNTQCTPGSGTFTSRNNHLPACLSCN 87

QY 64 VLGEREEERACHATHNRCRCRTGFF-----AHAGFCLEHASCPCPGAGVIAPGTPSQ 117
 DB 88 GRCSNQVETRSCNTHNRICECSFGYYCLLKSGSGCKACVSTQKCGIGYGV-SGHTSVG 146

QY 118 NTQCPCPPGTFSSSSSQOQPHRNCATGLALNVPSSSHDTLCTSGTGFPLSTRVP 177
 DB 147 DVICSPCGFGYSHTVSSADKCEPVNNTFNVIDEITLYPVNMTSCTRTTTTGLSESL 206

QY 178 GAE 180
 DB 207 TSE 209

RESULT 9
 B43692
 T2 protein - rabbit fibroma virus
 C:Species: rabbit fibroma virus, Shope fibroma virus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: B43692
 R:Upton, C.; Delange, A.M.; McPadden, G.
 Virology 160, 20-30, 1987
 A:Title: Tumorigenic poxviruses: genomic organization and DNA sequence of the telomeric
 A:Reference number: A43692; MUID:87321103; PMID:2826128
 A:Accession: B43692
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-325 <UPT>
 A:Cross-references: GB:M17433
 C:Superfamily: myxoma virus T2 protein; NGF receptor repeat homology
 P:64-105/Domain: NGF receptor repeat homology <NG2>
 P:106-147/Domain: NGF receptor repeat homology <NG3>

Query Match 15.7%; Score 234.5; DB 2; Length 325;
 Best Local Similarity 32.9%; Pred. No. 1.5e-10;
 Matches 52; Conservative 19; Mismatches 76; Indels 11; Gaps 3;

QY 18 LVCAQCPCPGTFVQPCRDSPPTTCGCPPRHYTOFWNYLRCRYCNVLGEREEERACH 77
 DB 38 LCCASCHPGFYASRLCGPGSNVCSPCBDGTFTASTNHAPACVSCRGCTGHLSSQPCD 97

QY 78 ATHNRCRCRTGFFA-----HAGFCLEHASCPCPGAGVIAPGTPSQNTQCPCPGTGA 131
 DB 98 RTHDRVCNCTGNYCLLKQNGCRICAPQTKCPAGYGV-SGHTAGDTLCEKCPPTYS 156

QY 132 SSSSQOQPHRNCATGLALNVPSSSHDTLCTSGT 169
 DB 157 SLSPTRCCTSPNYISVGFNL-----YFVNETSCITTAG 190

RESULT 10
 I37552
 Qx40 homolog - human
 C:Species: Homo sapiens (man)
 C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 11-Jan-2000
 C:Accession: I37552
 R:Latzka, U.; Darkop, H.; Schmittger, S.; Ringeling, J.; Eitelbach, F.; Hummel, M.; Fona
 Eur. J. Immunol. 24, 677-683, 1994

Best Local Similarity 30.4%; Pred. No. 9.6e-09;
Matches 46; Conservative 19; Mismatches 80; Indels 11; Gaps 3;

QY 18 LVCAQCPGTFVQPCRDSPPTTCGPPPHYTQFVNYLERCRVNCVLCGEREAEARACH 77
Db 38 LCTSCPPGVSASLQCGSDTWCSCKNETFTASTHAPACVSCRGCTGHLSESQSD 97
QY 78 ATHNRACRCRTGFFA-----HAGFCLHASCPPGAGVIAPGTPSQNTQCPQPPGTFSA 131
Db 98 KTRDEVCCSAGNYCLLKQGBGCRICAPKTKCPAGYGV-SCHTRTGDLVCTKCPRYTSD 156
QY 132 SSSSEQCQPHRNCALGLALNVPGSSSHDITLCTSCGTG 159
Db 157 AVSSTETCTSFNYISVEFNL-----YFVNFTSCTTAG 190

RESULT 14

A46476
B cell-associated surface molecule CD40, long splice form - mouse
C:Species: Mus musculus (house mouse)
C:Date: 18-Jun-1993 #sequence_revision 18-Nov-1994 #text_change 17-Nov-2003
C:Accession: A46476; A46515
R:Torres, R.M.; Clark, E.A.
J. Immunol. 148, 620-626, 1992
A:Title: Differential increase of an alternatively polyadenylated mRNA species of murine CD40
A:Reference number: A46476; MUID:9205763; PMID:1370315
A:Accession: A46476
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-305 <TOR>
A:Cross-references: GB:M83312; NID:gl553058
A:Note: sequence extracted from NCBI backbone (NCBIN:75206, NCBIP:75207)
A:Note: this translation is not annotated in GenBank entry MUSCD40A, release 113.0
R:Grimaldi, J.C.; Torres, R.; Kozak, C.A.; Chang, R.; Clark, E.A.; Howard, M.; Cockayne, R.; Immunol. 149, 3921-3926, 1992
A:Title: Genomic structure and chromosomal mapping of the murine CD40 gene.
A:Reference number: A46515; MUID:93094586; PMID:1281194
A:Accession: A46515
A:Status: preliminary; not compared with conceptual translation
A:Molecule type: nucleic acid
A:Residues: 1-287, 'LV' <GRI>
A:Cross-references: GB:M83312; NID:gl553058; PIDN:AAB08705.1; PID:gl553059; GB:M94126; NCBIP:120357
A:Experimental source: BAB/c, liver
A:Note: sequence extracted from NCBI backbone (NCBIP:120357)
C:Comment: For an alternative splice form, see PIR:A46515.
C:Comment: For an alternative splice form, see PIR:A46476.
C:Superfamily: CD27 antigen; NGF receptor repeat homology
C:Keywords: alternative splicing; transmembrane protein
F:105-144/Domain: NGF receptor repeat homology <NGF>

Query Match 13.6%; Score 203; DB 2; Length 305;
Best Local Similarity 31.1%; Pred. No. 3.3e-08;
Matches 47; Conservative 19; Mismatches 77; Indels 8; Gaps 3;

QY 20 CAQCPGTFVQPCRDSPPTTCGPPPHYTQFVNYLERC---RYCNVLCGEREAEARAC 76
Db 38 CDLCQPGSRLTSHCTALEXTQCHDSGEFSQWNRRETRCHQHRCEPNQGLRVKKEGT- 96
QY 77 HATHNRACRCRTGFFA---HAGFCLHASCPPGAGVIAPGTPSQNTQCPQPPGTFSSA 133
Db 97 -AESTVTCCKSGQCHTSKDCACAGHTFCITFGVGMENATETDITVCHPCPVGFESNQ 155
QY 134 SSSSEQCQPHRNCALGLALNVPGSSSHDITLC 164
Db 156 SLFECYPWTSCEKXNLEVLQKGTSGTNVIC 186

RESULT 15

I48700
gene ox40 protein - mouse
N:Alternate names: Ox40 antigen
C:Species: Mus musculus (house mouse)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #ext_change 11-Jan-2003

C:Accession: I48700; I48334; S34377
R:Calderhead, D.M.; Buhmann, J.E.; van den Bortwegh, A.J.; Claassen, E.; Noelle, R.J.; J. Immunol. 151, 5261-5271, 1993
A:Title: Cloning of mouse Ox40: a T cell activation marker that may mediate T-B cell in A:Reference number: I48700; MUID:94044750; PMID:8228223
A:Accession: I48700
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-272 <RES>
A:Cross-references: EMBL:Z21674; NID:9312827; PIDN:CAA79772.1; PID:9312828
R:Birkeland, M.L.; Copeland, N.G.; Gilbert, D.J.; Jenkins, N.A.; Barclay, A.N. Eur. J. Immunol. 25, 926-930, 1995
A:Title: Gene structure and chromosomal localization of the mouse homologue of rat Ox40 A:Reference number: I48334; MUID:95255413; PMID:7737295
A:Accession: I48334
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-14, 'G', 16-272 <RE2>
A:Cross-references: EMBL:X85214; NID:g732818; PIDN:CAA59476.1; PID:g732819
C:Genetics:
A:Gene: ox40
A:Introns: 45/1; 86/1; 122/1; 144/2; 210/1; 250/1
C:Superfamily: CD27 antigen; NGF receptor repeat homology

Query Match 13.0%; Score 194.5; DB 2; Length 272;
Best Local Similarity 30.4%; Pred. No. 1.3e-07;
Matches 51; Conservative 16; Mismatches 58; Indels 43; Gaps 8;

QY 6 TYPWRDAETGERLVCAQCPGTFVQPCRDSPPTTCGPPPHYTQFVNY--LERCRYCN 63
Db 31 TYP-----SGHK-CCRECQPGHGMVSRCDHTRTDILCHPCETGTYNEAVNYDTCKQCTQCN 84
QY 64 VLCGEREAEARACHATHNRACRCRTGFFAHAGFCLHASCPPGAGVIAPGT-PSQNT--- 119
Db 85 HRSQ--SELKONCTPTQTVTCRCR-----PQTPRQDSGYK 118
QY 120 ---QCQCPGTFSSASSSSSQCPHRNCTALGLALNVPGSSSHDITLC 164
Db 119 LGVDCVPCPPGHP--SPGNQACKPWTNCTLSGKQTRHEASDLSDAVC 164

Search completed: December 3, 2003, 13:14:38
Job time : 21 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2003, 13:07:31 ; Search time 17 Seconds

(Without alignments)
749.661 Million cell updates/sec

Title: US-10-069-385-1

Perfect score: 1.491

Sequence: 1 VAETPTYPWRDAETGERLVC.....RVARYPGIERSVRERFLPVH 271

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1491	400.0	300	1 TR6B_HUMAN	O95407 homo sapien
2	440.5	29.5	401	1 T11B_HUMAN	O00300 homo sapien
3	425.5	28.5	401	1 T11B_RAT	O08727 rattus norv
4	424.5	28.5	401	1 T11B_MOUSE	O08712 mus musculus
5	340.5	22.8	461	1 T11B_HUMAN	P20333 homo sapien
6	332.5	22.3	474	1 T11B_MOUSE	P25119 mus musculus
7	299.5	20.1	435	1 TNR3_HUMAN	P36941 homo sapien
8	286.5	19.3	655	1 TR21_MOUSE	Q96945 mus musculus
9	287	19.2	655	1 TR21_HUMAN	C75509 homo sapien
10	265.5	17.8	415	1 TNR3_MOUSE	P50284 mus musculus
11	260	17.4	349	1 CRMB_VARV	P34015 variola vir
12	257.5	17.3	349	1 CRMB_CAMP	Q84947 camelpox vi
13	254.5	17.1	351	1 CRMB_COMPX	Q73559 cowpox viru
14	244	16.4	283	1 TR14_HUMAN	Q92956 homo sapien
15	235.5	15.8	616	1 T111_HUMAN	Q95666 homo sapien
16	234.5	15.7	325	1 VT2_SFVKA	P25943 Shope fibro
17	220.5	14.8	625	1 T111_MOUSE	O35305 mus musculus
18	215.5	14.5	277	1 TNR4_HUMAN	P43489 homo sapien
19	211.5	14.2	271	1 TNR4_RAT	P15725 rattus norv
20	211	14.2	277	1 TNR5_HUMAN	P25942 homo sapien
21	210.5	14.1	326	1 VT2_MTXVL	P29825 myxoma viru
22	203	13.6	289	1 TNR5_MOUSE	P27512 mus musculus
23	202	13.5	269	1 TNR5_BOVIN	Q28203 bos taurus
24	194.5	13.0	272	1 TNR4_MOUSE	P47741 mus musculus
25	185	12.4	256	1 TNR9_MOUSE	P20334 mus musculus
26	182	12.2	595	1 TNR8_HUMAN	P28908 homo sapien
27	174	11.7	255	1 TNR9_HUMAN	Q07011 homo sapien
28	171.5	11.5	416	1 TR16_CHICK	P18519 gallus gall
29	171	11.5	480	1 TR22_MOUSE	Q96962 mus musculus
30	168	11.3	425	1 TR16_RAT	P07174 rattus norv
31	163	10.9	332	1 TNR6_PIG	Q77736 sus scrofa
32	162	10.9	417	1 TR16_MOUSE	Q92041 mus musculus
33	158	10.6	427	1 TR16_HUMAN	P08138 homo sapien

RESULT 1

ID	TR6B_HUMAN	STANDARD;	PRT;	300 AA.
AC	O95407;			
DT	28-FEB-2003 (Rel. 41, Last sequence update)			
DT	15-SEP-2003 (Rel. 42, Last annotation update)			
DE	Tumor necrosis factor receptor superfamily member 6B precursor (Decoy receptor for Fas ligand) (Decoy receptor 3) (DCR3) (M68).			
GN	TNFRSF6B OR DCR3 OR TR6.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Fetal lung;			
RX	MEDLINE=99087326; PubMed=9872321;			
RA	Pitti R.M., Marsters S.A., Lawrence D.A., Roy M., Kischkel F.C., Dowd P., Huang A., Donahue C.J., Sherwood S.W., Baldwin D.T., Godowski P.J., Wood W.I., Gurney A.L., Hillan K.J., Cohen R.L., Goddard A.D., Botstein D., Ashkenazi A.;			
RA	*Genomic amplification of a decoy receptor for Fas ligand in lung and colon cancer.;			
RT	Nature 396:699-703 (1998).			
RL	[2]			
RN	SEQUENCE FROM N.A., AND SEQUENCE OF 30-35.			
RP	TISSUE=Prostate;			
RC	MEDLINE=99253915; PubMed=10318773;			
RX	Yu K.-Y., Kwon B., Ni J., Zhai Y., Ebner R., Kwon B.S.;			
RA	*A newly identified member of tumor necrosis factor receptor superfamily (TR6) suppresses LIGHT-mediated apoptosis.;			
RT	J. Biol. Chem. 274:13733-13736(1999).			
RL	[3]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Lung;			
RC	MEDLINE=20122600; PubMed=10655513;			
RX	Bai C., Connolly B., Metzker M.L., Hilliard C.A., Liu X., Sandig V., Soderman A., Galloway S.M., Liu Q., Austin C.P., Caskey C.T.;			
RA	*Overexpression of M68/DCR3 in human gastrointestinal tract tumors independent of gene amplification and its location in a four-gene cluster.;			
RT	Proc. Natl. Acad. Sci. U.S.A. 97:1230-1235(2000).			
RL	[4]			
RN	SEQUENCE FROM N.A.			
RP	Matthews L.;			
RL	Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.			
RL	[5]			
RN	SEQUENCE FROM N.A.			
RP	TISSUE=Lung, and Skin;			
RC	MEDLINE=22388257; PubMed=12477932;			
RX	Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Schuler G.D., Klausner R.D., Collins F.S., Wagner K.H., Schaefer C.F., Bhat N.K., Altschul S.P., Zeeberg B., Buetow K.H., Moore T., Max S.I., Wang J., Hsieh P., Hopkins R.F., Jordan H., Moore T., Farmer A.A., Rubin G.M., Hong L., Diatchenko L., Marusina K.,			

34	155.5	10.4	327	1	TNR6_MOUSE	P25446 mus musculus
35	155	10.4	323	1	TNR6_BOVIN	P51867 bos taurus
36	153	10.3	241	1	TR18_HUMAN	Q9Y5U5 homo sapien
37	152.5	10.2	430	1	TRLT_MACEA	Q9N092 macaca fasc
38	151.5	10.2	430	1	TRLT_HUMAN	Q96924 homo sapien
39	148.5	10.0	176	1	TR23_MOUSE	Q96963 mus musculus
40	148	9.9	250	1	TNR7_MOUSE	P41272 mus musculus
41	147.5	9.9	5376	1	ZAN_MOUSE	O88799 mus musculus
42	145	9.7	335	1	TNR6_HUMAN	P25445 mus musculus
43	143.5	9.6	471	1	TR1A_BOVIN	O19131 bos taurus
44	142.5	9.6	260	1	TNR7_HUMAN	P26842 homo sapien
45	137.5	9.2	324	1	TNR6_RAT	Q63199 rattus norv

ALIGNMENTS

Query Match	100.0%	Score 1491	DB 1	Length 300
Best local similarity	100.0%	Pred. No. 1.9e-108		
Matches 271	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	VAETPTYPNRDAETGRLVCAQC	PGTFFVORPCRDSPTTCGCP	PRHYTQFWNYLECR 60
DB	30	VAETPTYPNRDAETGRLVCAQC	PGTFFVORPCRDSPTTCGCP	PRHYTQFWNYLECR 89
QY	61	YCNVLGGEREEEARACHATHNRA	CRCTGTFFAHAGFCLEHASCE	PPGAGVIAPGTFSQNTQ 120
DB	90	YCNVLGGEREEEARACHATHNRA	CRCTGTFFAHAGFCLEHASCE	PPGAGVIAPGTFSQNTQ 149
QY	121	CQCPPTGTTASSSSSQCPHNC	TALGLALNVPSSSHDTLTCT	SGTGPPLSTRVFGAE 180
DB	150	CQCPPTGTTASSSSSQCPHNC	TALGLALNVPSSSHDTLTCT	SGTGPPLSTRVFGAE 209
QY	181	ECERAVIDFVAFODISIKRL	ORLLQALAEPEGGPTPRAG	RAALQKLRRRLTELGAQD 240
DB	210	ECERAVIDFVAFODISIKRL	ORLLQALAEPEGGPTPRAG	RAALQKLRRRLTELGAQD 269
QY	241	GALLVRLQLQALVARMPGLS	RVREFLPVH 271	
DB	270	GALLVRLQLQALVARMPGLS	RVREFLPVE 300	

RESULT 2

T11B HUMAN STANDARD; PRT; 401 AA.

AC CQ030; Q06236; Q0UHP4;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE Tumor necrosis factor receptor superfamily member 11B precursor (osteoprotegerin) (osteoclastogenesis inhibitory factor).

GN TNFRSF11B OR OPG OR OCIF.

OS Homo sapiens (Human).

OC Buckyryoka; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Kidney;

EX MEDLINE=97262071; PubMed=9108485;

RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S., Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G., Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J., Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W., Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R., Suggs S., Boyle W.J.;

RA "osteoprotegerin: a novel secreted protein involved in the regulation of bone density.";

RT Cell 89:309-319(1997).

RL [2]

RN SEQUENCE FROM N.A.

RP TISSUE=Lung cancer;

RC MEDLINE=98151033; PubMed=9492069;

RA Yasuda H., Shima N., Nakagawa N., Mochizuki S.-I., Yano K., Fujise N., Sato Y., Goro M., Yamaguchi K., Kuriyama M., Kanno T., Murakami A., Tsuda E., Morinaga T., Higashio K.;

RA "Identity of osteoclastogenesis inhibitory factor (OCIF) and osteoprotegerin (OPG): a mechanism by which OPG/OCIF inhibits osteoclastogenesis in vitro.";

RT Endocrinology 139:1329-1337(1998).

RL [3]

RN SEQUENCE FROM N.A., AND VARIANT ASN-3.

RP TISSUE=Placenta;

RC MEDLINE=98351569; PubMed=9688283;

RA Morinaga T., Nakagawa N., Yasuda H., Tsuda E., Higashio K.;

RA "cloning and characterization of the gene encoding human osteoprotegerin/osteoclastogenesis-inhibitory factor.";

RT Eur. J. Biochem. 254:685-691(1998).

RL [4]

RN SEQUENCE FROM N.A., AND VARIANT ASN-3.

CC TISSUE=Eye;
RX MEDLINE=22389257; PubMed=12477932;
RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavart T.L., Scheetz T.E.,
RA Brownstein M.O., Ustin T.B., Toshlyuki S., Carninci P., Prange C.,
RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulláhy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [5]
RP SEQUENCE OF 22-36 AND 378-401.
RX MEDLINE=98238645; PubMed=9571159;
RA Tomoyasu A., Goto X., Fujise N., Mochizuki S.-I., Yasuda H.,
RA Morinaga T., Tsuda E., Higashio K.;
RT "Characterization of monomeric and homodimeric forms of
RT osteoclastogenesis inhibitory factor.";
RL Biochem. Biophys. Res. Commun. 245:382-387 (1998).
RN [6]
RP SEQUENCE OF 22-393 FROM N.A.
RC TISSUE=Placenta;
RA He Z.-Y., Yang G.-Z., Zhang W.-J., Wu X.-F.;
RT "Cloning and expression of osteoprotegerin from Homo sapiens.";
RL Acta Biochim. Biophys. Sin. 31:680-684 (1999).
RN [7]
RP SEQUENCE OF 242-255; 354-359 AND 369-378, AND FUNCTION.
RX MEDLINE=97312536; PubMed=9168977;
RA Tsuda E., Goto M., Mochizuki S.-I., Yano K., Kobayashi F.,
RA Morinaga T., Higashio K.;
RT "Isolation of a novel cytokine from human fibroblasts that
RT specifically inhibits osteoclastogenesis.";
RL Biochem. Biophys. Res. Commun. 234:137-142 (1997).
RN [8]
RP TRAIL BINDING.
RX MEDLINE=98269100; PubMed=9603945;
RA Emery J.G., McDonnell P., Burke M.B., Deen K.C., Lyn S., Silverman C.,
RA Dul E., Appelbaum E.R., Eichman C., DiPrinzio R., Dodds R.A.,
RA James I.E., Rosenberg M., Lee J.C., Young P.R.;
RT "Osteoprotegerin is a receptor for the cytotoxic ligand TRAIL.";
RL J. Biol. Chem. 273:4363-4367 (1998).
RN [9]
RP CHARACTERIZATION, AND MUTAGENESIS OF CYS-400.
RX MEDLINE=98148058; PubMed=9478964;
RA Yanaguchi K., Kinosaki M., Goto M., Kobayashi F., Tsuda E.,
RA Morinaga T., Higashio K.;
RT "Characterization of structural domains of human osteoclastogenesis
RT inhibitory factor.";
RL J. Biol. Chem. 273:5117-5123 (1998).
RN [10]
RP REVIEW
RX MEDLINE=21395914; PubMed=11505389;
RA Hofbauer L.C., Neubauer A., Heufelder A.E.;
RT "Receptor activator of nuclear factor-kappaB ligand and
RT osteoprotegerin: potential implications for the pathogenesis and
RT treatment of malignant bone diseases.";
RL Cancer 92:463-470 (2001).
CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
CC its function in osteoclastogenesis. Inhibits the activation of
CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
CC play a role in preventing arterial calcification. May act as decoy

CC receptor for TRAIL and protect against apoptosis. TRAIL binding
CC blocks the inhibition of osteoclastogenesis.
CC -!- SUBUNIT: Homodimer.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in adult lung, heart, kidney,
CC liver, spleen, thymus, prostate, ovary, small intestine, thyroid,
CC lymph node, trachea, adrenal gland, testis, and bone marrow.
CC Detected at very low levels in brain, placenta and lung.
CC -!- INDUCTION: Upregulated by increasing calcium-concentration in the
CC medium and estrogens. Downregulated by glucocorticoids.
CC -!- PTM: N-glycosylated. Contains sialic acid residues.
CC -!- PTM: N-terminus may be blocked.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 2 death domains.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U94332; AAB53709.1; -;
CC EMBL: AB002146; BAA25910.1; -;
CC EMBL: AB008822; BAA32076.1; -;
CC EMBL: AB008821; BAA32076.1; JOINED.
CC EMBL: BC030155; AAB30155.1; -;
CC EMBL: AF134187; AAF20168.1; -;
CC HSP: P25942; ICDP.
CC Genew; HGNC:11909; TNFRSF11B.
CC MIM; 602643; -;
CC GO; GO:0005576; C:extracellular; TAS.
CC GO; GO:0005125; F:cytokine activity; TAS.
CC GO; GO:0004872; F:receptor activity; TAS.
CC GO; GO:0007165; P:signal transduction; TAS.
CC GO; GO:0001501; P:skeletal development; TAS.
CC InterPro; IPR000488; Death.
CC Pfam; PF0020; TNFR_c6; 3-
CC SMART; SM00005; DEATH; 1.
CC SMART; SM00208; TNFR; 4.
CC PROSITE; PS00017; DEATH_DOMAIN; FALSE_NEG.
CC PROSITE; PS00652; TNFR_NGFR_1; 1.
CC PROSITE; PS00500; TNFR_NGFR_2; 2.
CC Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
CC SIGNAL 1 21
CC CHAIN 22 401
CC TUMOR NECROSIS FACTOR RECEPTOR
CC SUPERFAMILY MEMBER 11B.
CC REPEAT 24 62
CC REPEAT 65 105
CC REPEAT 107 142
CC REPEAT 145 185
CC REPEAT 198 269
CC DOMAIN 270 365
CC SITE 400 400
CC INVOLVED IN DIMERIZATION.
CC DISULFID 41 54
CC BY SIMILARITY.
CC DISULFID 44 62
CC BY SIMILARITY.
CC DISULFID 65 80
CC BY SIMILARITY.
CC DISULFID 83 97
CC BY SIMILARITY.
CC DISULFID 107 118
CC BY SIMILARITY.
CC DISULFID 124 142
CC BY SIMILARITY.
CC DISULFID 145 160
CC BY SIMILARITY.
CC DISULFID 166 185
CC BY SIMILARITY.
CC CARBOHYD 98 98
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 152 152
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 165 165
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 178 178
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC CARBOHYD 289 289
CC N-LINKED (GLCNAC. .) (POTENTIAL).
CC VARIANT 3 3
CC K -> N
CC /FTId=VAR_013439.

```

FT MUTAGEN 400 400 C-S: ABOLISHES DIMERIZATION.
FT MUTAGEN 400 401 MISSING: ABOLISHES DIMERIZATION.
FT CONFLICT 263 263 D -> A (IN REF. 1).
SQ SEQUENCE 401 AA; 46040 MW; EDP448B67D86C71E CRC64;

Query Match
Best Local Similarity 41.2%; Pred. No. 4e-27; Length 401;
Matches 77; Conservative 31; Mismatches 74; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLIVCAQCPGTFVQPCRRDSTTCGPPRHYTFQWNYLRCRYCNV 64
DB 26 PKLYHYDEETSHQLCDKCPGGVILKQCHCTAKWKTVCAPCPDHYTDSWHSDECLYCS 85
QY 65 LCGEREERACHATHNRACRGTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQCP 124
DB 86 VKELQTVKQECNRTNHRVCEGRYLEFCLKHSRCPGGLVGLQAGTDERNTVCKRC 145
QY 125 PGTFSSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTSCGTFPLSTRVPGAEB-C 182
DB 146 PDGFFSETSSKAPCRKHTNCSSIGLLIQGNATHDNV---CSGNREATQCGIDVTLC 202
QY 183 ERAVIDFVAFODISIKRLQRLQAL 207
DB 203 EEAFFRVPKILPNWLSVLVDSL 227

RESULT 4
ID T11B MOUSE STANDARD; PRT; 401 AA.
AC 008712; 070202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
DE TNFRSF11B OR OPB OR OCIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

```

CC EXBL; U94330; AAB53707.1; -.
DR HGSP; P25942; 1CDF.
DR InterPro; IPR000488; Death.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS0017; DEATH DOMAIN; FALSE_NEG.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS0050; TNFR_NGFR_2; 2.
KW Cytokine; Apoptosis; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 21
FT CHAIN 22 401
TUMOR NECROSIS FACTOR RECEPTOR
SUPERFAMILY MEMBER 11B.
FT REPEAT 24 62
FT REPEAT 65 105
FT REPEAT 107 142
FT REPEAT 145 185
FT DOMAIN 198 269
FT DOMAIN 270 365
FT SITE 400 400
INVOLVED IN DIMERIZATION (BY SIMILARITY).
FT DISULFID 41 54
FT DISULFID 44 62
FT DISULFID 65 80
FT DISULFID 83 97
FT DISULFID 87 105
FT DISULFID 107 118
FT DISULFID 124 142
FT DISULFID 145 160
FT DISULFID 166 185
FT CARBOHYD 98 98
FT CARBOHYD 165 165
FT CARBOHYD 178 178
FT CARBOHYD 289 289
SQ SEQUENCE 401 AA; 46192 MW; PEC6A31FID4E573A CRC64;

Query Match
Best Local Similarity 28.5%; Score 425.5; DB 1; Length 401;
Matches 81; Conservative 33; Mismatches 86; Indels 5; Gaps 2;

QY 5 PTPWRDAETGERLIVCAQCPGTFVQPCRRDSTTCGPPRHYTFQWNYLRCRYCNV 64
DB 26 PKLYHYDEETGERQLCDKCAPGTYLKQCHCTVRRKTLVCFDYSYTDWHSDEVCYSP 85
QY 65 LCGEREERACHATHNRACRGTGFFAHAGFCLHASCPPGAGVIAPGTPSQNTQCP 124
DB 86 VKELQTVKQECNRTNHRVCEGRYLEFCLKHSRCPGGLVGLQAGTDERNTVCKRC 145
QY 125 PGTFSSASSSSSQCPHRNCTALGLALNVPSSSHDTLCTSCGTFPLSTRVPGAEB-C 182
DB 146 PDGFFSETSSKAPCRKHTNCSSIGLLIQGNATHDNV---CSGNREATQCGIDVTLC 202
QY 183 ERAVIDFVAFODISIKRLQRLQAL 207
DB 203 EEAFFRVPKILPNWLSVLVDSL 227

RESULT 4
ID T11B MOUSE STANDARD; PRT; 401 AA.
AC 008712; 070202;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11B precursor
DE (Osteoprotegerin) (Osteoclastogenesis inhibitory factor).
DE TNFRSF11B OR OPB OR OCIF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]

```

RP SEQUENCE FROM N.A.
 RC STRAIN-BALB/c; TISSUE=Kidney;
 RX MEDLINE=97262071; PubMed=9108485;
 RA Simonet W.S., Lacey D.L., Dunstan C.R., Kelley M., Chang M.-S.,
 RA Luethy R., Nguyen H.Q., Woodson S., Bennett L., Boone T., Shimamoto G.,
 RA Derose M., Elliott R., Colombero A., Tan H.-L., Trail G., Sullivan J.,
 RA Davy E., Bucay N., Renshaw-Gegg L., Hughes T.M., Hill D., Pattison W.,
 RA Campbell P., Sander S., Van G., Tarpley J., Derby P., Lee R.,
 RA Suggs S., Boyle W.J.;
 RT "Osteoprotegerin: a novel secreted protein involved in the regulation
 RT of bone density";
 RL Cell 89:309-319(1997).
 RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS PRO-138; ARG-161; ASP-165; ALA-288
 RP AND ARG-236.
 RC STRAIN=129/Ola, and NIH Swiss; TISSUE=Fibroblast;
 RX MEDLINE=98382527; PubMed=9714833;
 RA Mizuno A., Yurakami A., Nakagawa N., Yasuda H., Tsuda E., Morinaga T.,
 RA Higashio K.;
 RT "Structure of the mouse osteoclastogenesis inhibitory factor (OCIF)
 RT gene and its expression in embryogenesis";
 RL Gene 215:339-343(1998).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=21060987; PubMed=10952716;
 RA Min H., Morony S., Sarosi I., Dunstan C.R., Capparelli C., Scully S.,
 RA Van G., Kaufman S., Kostenuik P.J., Lacey D.L., Boyle W.J.,
 RA Simonet W.S.;
 RT "Osteoprotegerin reverses osteoporosis by inhibiting endosteal
 RT osteoclasts and prevents vascular calcification by blocking a process
 RT resembling osteoclastogenesis";
 RL J. Exp. Med. 192:463-474(2000).
 CC -!- FUNCTION: Acts as decoy receptor for RANKL and thereby neutralizes
 CC its function in osteoclastogenesis. Inhibits the activation of
 CC osteoclasts and promotes osteoclast apoptosis in vitro. Bone
 CC homeostasis seems to depend on the local RANKL/OPG ratio. May also
 CC play a role in preventing arterial calcification. May act as decoy
 CC receptor for TRAIL and protect against apoptosis. TRAIL binding
 CC blocks the inhibition of osteoclastogenesis.
 CC -!- SUBUNIT: Homodimer.
 CC -!- SUBCELLULAR LOCATION: Secreted.
 CC -!- TISSUE SPECIFICITY: Highly expressed in liver, lung, stomach,
 CC intestines and calvaria. Highly expressed in decidua and placenta,
 CC and in embryo.
 CC -!- DEVELOPMENTAL STAGE: Detected in embryo at high levels on day 7,
 CC whereas expression decreases at day 11 and increases from day 15
 CC to 17. On day 15 found in developing bone primordia,
 CC brachiocephalic artery and ductus arteriosus, left main bronchus,
 CC abdominal aorta and midgut.
 CC -!- INDUCTION: Upregulated by TGF-beta and estrogens. Downregulated by
 CC 1,25-dihydroxyvitamin D3 and parathyroid hormone.
 CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -!- SIMILARITY: Contains 2 death domains.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 CC -----
 CC EMBL: U94331; AB53708.1; -;
 CC EMBL: AB013898; BAA28269.1; -;
 CC EMBL: AB013903; BAA33388.1; -;
 CC EMBL: AB013899; BAA33388.1; JOINED.
 CC EMBL: AB013900; BAA33388.1; JOINED.
 CC EMBL: AB013901; BAA33388.1; JOINED.
 CC EMBL: AB013902; BAA33388.1; JOINED.
 CC HSSP: P25942; 1CDF.
 CC MG: MG1:109587; Tnfisfl1b.
 CC GO: GO:0005578; C:extracellular matrix; IDA.
 CC InterPro: IPR000488; Death.

DR InterPro: IPR001368; TNFR_C6.
 DR Pfam: PF00020; TNFR_C6; 3.
 DR SMART: SM00003; DEATH; 1.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS00017; DEATH DOMAIN; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS00652; TNFR_NGFR_2; 2.
 DR PROSITE: PS00652; TNFR_NGFR_3; 3.
 KW Receptor; Apoptosis; Glycoprotein; Repeat; Signal; Polymorphism.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 401 TUMOR NECROSIS FACTOR RECEPTOR
 FT SUPERFAMILY MEMBER 11B.
 FT REPEAT 24 62 TNFR-CYS 1.
 FT REPEAT 65 105 TNFR-CYS 2.
 FT REPEAT 107 142 TNFR-CYS 3.
 FT REPEAT 145 185 TNFR-CYS 4.
 FT DOMAIN 198 269 DEATH 1.
 FT DOMAIN 283 365 DEATH 2.
 FT SITE 400 400 INVOLVED IN DIMERIZATION (BY SIMILARITY).
 FT DISULFID 41 54 BY SIMILARITY.
 FT DISULFID 44 62 BY SIMILARITY.
 FT DISULFID 65 80 BY SIMILARITY.
 FT DISULFID 83 97 BY SIMILARITY.
 FT DISULFID 87 105 BY SIMILARITY.
 FT DISULFID 107 118 BY SIMILARITY.
 FT DISULFID 124 142 BY SIMILARITY.
 FT DISULFID 145 160 BY SIMILARITY.
 FT DISULFID 166 185 BY SIMILARITY.
 FT CARBOHYD 98 98 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 165 165 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 138 138 R -> P (IN STRAINS 129/OLA AND NIH
 FT SWISS).
 FT VARIANT 161 161 I -> R (IN STRAINS 129/OLA AND NIH
 FT SWISS).
 FT VARIANT 165 165 N -> D (IN STRAINS 129/OLA AND NIH
 FT SWISS).
 FT VARIANT 288 288 S -> A (IN STRAINS 129/OLA AND NIH
 FT SWISS).
 FT VARIANT 296 296 L -> R (IN STRAINS 129/OLA AND NIH
 FT SWISS).
 SQ SEQUENCE 401 AA; 45923 MW; CAA6102D3B312470 CRC64;
 Query Match 28.5%; Score 424.5; DB 1; Length 401;
 Best Local Similarity 39.0%; Pred. No. 78-26;
 Matches 80; Conservative 32; Mismatches 88; Indels 5; Gaps 2;
 QY 5 PTYPWRDAETGERLVCAOCPGTFVQRPQRDSPTTCGPPRHVTFQWNYLERCRYCNV 64
 DB 26 KYLHYDETHGQLLCKKCAPCTYLKQHTVVRKTLVCPDHSYDTSWHTSDCYVCSP 85
 QY 65 LCGEREERARACHATHNRCRCRTGFFAHAGFCLEHACGPGAGVIAPTGPTQNTQCP 124
 DB 86 VKELQSVKQECNRTHNRVCECEGRYLEIEFLKHSRCPGSGVVOAGTPTNRTVCKKC 145
 QY 125 PPGFPSASSSSEQOPHNCNCTALGALNVPSSSHDTLTCTGTFPLSTRVPGAE--C 182
 DB 146 PDGFPSTGSKAPCIKNTNCSTPGLLTIQGNATHDNV---CSGNREATQKGDVTLIC 202
 QY 183 ERAVIDFVAFQDISIKRLQLQAL 207
 DB 203 EAAPFRFAVPTKLIIPWLSVLVDSL 227
 RESULT 5
 TRIB HUMAN
 ID TRIB HUMAN STANDARD; PRT; 461 AA.
 AC P20333; Q16042; QYUHI;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 18 precursor (Tumor
 DE necrosis factor receptor 2) (p80) (TNF-R2) (p75) (CD120b) (Stanecept)

[Contains: Tumor necrosis factor binding protein 2 (TNF2)].

DR TNFRSF1B OR TNFR2 OR TNFR.

GN Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1].

RN SEQUENCE FROM N.A.

RP MEDLINE=90260639; PubMed=2160731;

RX MEDLINE=90260639; PubMed=2160731;

RA Kohno T., Brewer M.T., Anderson D., Solam L., Beckmann M.P., Jerzy R.,

RA Smith C.A., Davis T., Cosman D., Goodwin R.G.;

RA Dower S.K., Cosman D., Goodwin R.G.;

RT "A receptor for tumor necrosis factor defines an unusual family of

RT cellular and viral proteins.";

RL Science 248:1019-1023(1990).

RN [2].

RN SEQUENCE FROM N.A., AND VARIANT ARG-196.

RP MEDLINE=91045991; PubMed=2172983;

RX MEDLINE=91045991; PubMed=2172983;

RA Kohno T., Brewer M.T., Baker S.L., Schwartz P.E., King M.W.,

RA Hale K.K., Squires C.H., Thompson R.C., Vannice J.L.;

RT "A second tumor necrosis factor receptor gene product can shed a

RT naturally occurring tumor necrosis factor inhibitor.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:8331-8335(1990).

RN [3].

RN SEQUENCE FROM N.A.

RP MEDLINE=96299745; PubMed=8661109;

RX MEDLINE=96299745; PubMed=8661109;

RA Beltinger C.P., White P.S., Maris J.M., Sulman E.P., Jensen S.J.,

RA Lepaslier D., Stallard B.J., Goeddel D.V., Desauvage F.J.,

RA Brodeur G.W.;

RT "Physical mapping and genomic structure of the human TNFR2 gene.";

RL Genomics 35:94-100(1996).

RN [4].

RN SEQUENCE OF 37-461 FROM N.A.

RP MEDLINE=91370690; PubMed=2166549;

RX MEDLINE=91370690; PubMed=2166549;

RA Dembic Z., Loetscher H., Gubler J., Pan Y.C., Lahm H.-W., Gentz R.,

RA Brockhaus M., Lesslauer W.;

RT "Two human TNF receptors have similar extracellular, but distinct

RT intracellular, domain sequences.";

RL Cytokine 2:231-237(1990).

RN [5].

RN SEQUENCE OF 16-461 FROM N.A., PARTIAL SEQUENCE, ANT. VARIANT ARG-196.

RP MEDLINE=9349572; PubMed=2166946;

RX MEDLINE=9349572; PubMed=2166946;

RA Heller R.A., Song K., Onasch M.A., Fischer W.H., Chang D.,

RA Ringold G.M.;

RT "Complementary DNA cloning of a receptor for tumor necrosis factor

RT and demonstration of a shed form of the receptor.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:6151-6155(1990).

RN [6].

RN SEQUENCE OF 154-183 FROM N.A., AND VARIANTS ARG-196 AND LYS-232.

RP MEDLINE=21069356; PubMed=11197692;

RX MEDLINE=21069356; PubMed=11197692;

RA Tsuchiya N., Komata T., Matsushita M., Ohashi J., Tokunaga K.;

RT "New single nucleotide polymorphisms in the coding region of human

RT TNFR2: association with systemic lupus erythematosus.";

RL Genes Immun. 1:501-503(2000).

RN [7].

RN SEQUENCE OF 27-31.

RP MEDLINE=90110215; PubMed=2153136;

RX MEDLINE=90110215; PubMed=2153136;

RA Engelmann H., Novick D., Wallach D.;

RT "Two tumor necrosis factor-binding proteins purified from human

RT urine. Evidence for immunological cross-reactivity with cell surface

RT tumor necrosis factor receptors.";

RL J. Biol. Chem. 265:1531-1536(1990).

RN [8].

RN SEQUENCE OF 23-40; 65-69; 136-141; 300-306 AND 346-362.

RP MEDLINE=91056048; PubMed=2173696;

RX MEDLINE=91056048; PubMed=2173696;

RA Loetscher H., Schlaeger E.J., Lahm H.-W., Pan Y.-C.E., Lesslauer W.,

RA Brockhaus M.;

RT "Purification and partial amino acid sequence analysis of two

RT distinct tumor necrosis factor receptors from HL60 cells.";

RL J. Biol. Chem. 265:20131-20138(1990).

RN [9].

RN CHARACTERIZATION.

RP MEDLINE=93016040; PubMed=1328224;

RX MEDLINE=93016040; PubMed=1328224;

RA Pennica D., Lam V.T., Mize N.K., Weber R.F., Lewis M., Fendly B.M.,

RA

Lipari M.T., Goeddel D.V.;

RT "Biochemical properties of the 75-kDa tumor necrosis factor receptor.

RT Characterization of ligand binding, internalization, and receptor

RT phosphorylation.";

RL J. Biol. Chem. 267:21172-21178(1992).

RN [10].

RN INTERACTION WITH TRAF2.

RP MEDLINE=94349371; PubMed=8069916;

RX MEDLINE=94349371; PubMed=8069916;

RA Roche M., Wong S.C., Henzel W.J., Goeddel D.V.;

RT "A novel family of putative signal transducers associated with the

RT cytoplasmic domain of the 75 kDa tumor necrosis factor receptor.";

RL Cell 78:681-692(1994).

RN [11].

RN X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 419-428 IN COMPLEX WITH

RP TRAF2.

RX MEDLINE=99221490; PubMed=10206649;

RX MEDLINE=99221490; PubMed=10206649;

RA Park Y.C., Burkitt V., Villa A.R., Tong L., Wu H.;

RT "Structural basis for self-association and receptor recognition of

RT human TRAF2.";

RL Nature 398:533-538(1999).

CC -!- FUNCTION: Receptor with high affinity for TNFRSF2/TNF-alpha and

CC approximately 5-fold lower affinity for homotrimeric

CC TNFRSF1/lymphotoxin-alpha. The TRAF1/2 complex recruits the

CC apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2.

CC -!- SUBUNIT: Binds to TRAF2.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein and secreted.

CC -!- PM: Phosphorylated; mainly on serine residues and with a very low

CC level on threonine residues.

CC -!- PM: A soluble form (tumor necrosis factor binding protein 2) is

CC produced from the membrane form by proteolytic processing.

CC -!- PHARMACEUTICAL: Available under the name Enbrel (Immunex and

CC Wyeth-Ayerst). Used to treat moderate to severe rheumatoid

CC arthritis (RA). Enbrel consist of the extracellular ligand-binding

CC portion of TNFR2 linked to an immunoglobulin Fc chain. It binds to

CC TNF-alpha and blocks its interactions with receptors.

CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.

CC -!- DATABASE: NAME=PRO; NOTE=CD guide: CD120b entry;

CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd120b.htm".

CC -!- DATABASE: NAME=Enbrel; NOTE=Clinical information on Enbrel;

CC WWW="http://www.enbrel.com/".

CC

This SWISS-PROT entry is copyright. It is produced through a collaboration

between the Swiss Institute of Bioinformatics and the EMBL outstation -

the European Bioinformatics Institute. There are no restrictions on its

use by non-profit institutions as long as its content is in no way

modified and this statement is not removed. Usage by and for commercial

entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

or send an email to license@isb-sib.ch).

EMBL; M32315; AAC59929.1; -

EMBL; U52165; AAC50622.1; -

EMBL; U52156; AAC50622.1; JOINED.

EMBL; U52157; AAC50622.1; JOINED.

EMBL; U52158; AAC50622.1; JOINED.

EMBL; U52159; AAC50622.1; JOINED.

EMBL; U52160; AAC50622.1; JOINED.

EMBL; U52161; AAC50622.1; JOINED.

EMBL; U52162; AAC50622.1; JOINED.

EMBL; U52163; AAC50622.1; JOINED.

EMBL; U52164; AAC50622.1; JOINED.

EMBL; M55994; AAA36755.1; -

EMBL; S63368; AAB19824.2; -

EMBL; M35857; AAB63262.1; -

EMBL; AB030950; BAA89053.1; -

PIR; A35356; A35356.

PDB; 1CA9; 12-APR-99.

Genew; HGNC:11917; TNFRSF1B.

MIM; 191191; -

GO; GO:0005031; F:tumor necrosis factor receptor activity; TAS.

InterPro; IPR001368; TNFR_c6.

Pfam; PF00020; TNFR_c6; 4.

SMART; SM00208; TNFR; 4.

PROSITE; PS00652; TNFR_NGFR_1; 2.

FT DISULFID 79 94 BY SIMILARITY.
 FT DISULFID 97 111 BY SIMILARITY.
 FT DISULFID 101 119 BY SIMILARITY.
 FT DISULFID 121 127 BY SIMILARITY.
 FT DISULFID 136 145 BY SIMILARITY.
 FT DISULFID 139 163 BY SIMILARITY.
 FT DISULFID 166 181 BY SIMILARITY.
 FT CARBOHYD 69 69 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 195 195 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 474 AA; 50319 MW; 462EAE398C4D6563 CRC64;
 Query Match 22.3%; Score 332.5; DB 1; Length 474;
 Best Local Similarity 29.7%; Pred. No. 1.1e-18;
 Matches 83; Conservative 44; Mismatches 109; Indels 39; Gaps 9;
 QY 17 RLVAQCPGFTVQRCRRDPTTCGPPRHYTFWNLERCYCNVLCGEREEARAC 76
 DB 52 QMCCAKCPGQYVRFHFNKTSIDTVACDCEASMYQVMNQPTCLSCSSCTTDQVEIRAC 111
 QY 77 HATHNRACRTGTGF-----AHAGF---CLEHACPPGAGVAPGTPTSONTCQCPPGTF 129
 DB 112 TKQNRVCAACBAGRYCALKTHSGRCQCMRLSKCGPGFGVASSRAPGNVLCRACAPGTF 171
 QY 130 SASSSSEQCPHRNCTALGALNWPSSSHDTLCT----SCTGFPILSTRVPGAECERA 185
 DB 172 SDTSTSDVCPHICSLA----IPGNASIDVAPESPTLSAIPRTLYVSQEPPTRSQ 227
 QY 186 VDFVAFQDISIKRLQRLQALQALPEGWGTPP-----RAGRAALQLKRLRRLTELLGAQD 240
 DB 228 PLD-----QEPGSPSTPSILSL-----GSTPIEQSTKGISLPIGLIVGVTSL----- 272
 QY 241 GALLVRLQLA-----RVARMEGLERSVREPLP 269
 DB 273 GLEMLGLVNCILLVQKKPSCLQDRAKVHPV 305

RESULT 7

INR3_HUMAN STANDARD; PRT; 435 AA.
 AC 236941;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (lymphotoxin-beta receptor) (Tumor necrosis factor receptor 2 related
 DE protein) (Tumor necrosis factor C receptor).
 GN LTRB OR TNFRSF3 OR TNFCR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RX MEDLINE=93252381; PubMed=8486360;
 RA Baens M., Chaffanet M., Cassiman J.J., den Berghe H., Marynen P.;
 RA "Construction and evaluation of a hncDNA library of human 12p
 RA transcribed sequences derived from a somatic cell hybrid";
 RL Genomics 16:214-218 (1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Yarushina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavate T.D., Scheetz T.E.,
 RA Brownstein M.J., Udell T.S., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.C., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smallos D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Mair M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [3]
 RP FUNCTION.
 RX MEDLINE=94225209; PubMed=8171323;
 RA Crowe P.D., Vanarsdale T.L., Walter B.N., Ware C.F., Hession C.,
 RA Ehrenfels B., Browning J.L., Din W.S., Goodwin R.G., Smith C.A.;
 RT "A lymphotoxin-beta-specific receptor";
 RL Science 264:707-710 (1994).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=9523511; PubMed=10207006;
 RA Wu M.-Y., Wang P.-Y., Han S.-H., Hsieh S.-L.;
 RT "The cytoplasmic domain of the lymphotoxin-beta receptor mediates cell
 RT death in HeLa cells";
 RL J. Biol. Chem. 274:11868-11873 (1999).
 RN [5]
 RP FUNCTION.
 RX MEDLINE=20261554; PubMed=10799510;
 RA Rooney I.A., Butrovich K.D., Glass A.A., Borboroglu S., Benedict C.A.,
 RA Whitbeck J.C., Cohen G.H., Eisenberg R.J., Ware C.F.;
 RT "The lymphotoxin-beta receptor is necessary and sufficient for
 RT LIGHT-mediated apoptosis of tumor cells";
 RL J. Biol. Chem. 275:14307-14315 (2000).
 RN [6]
 RP INTERACTION WITH TRAF3.
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT "TRAF5, an activator of NF-kappaB and putative signal transducer for
 RT the lymphotoxin-beta receptor";
 RL C. Biol. Chem. 271:14661-14664 (1996).
 RN [7]
 RP INTERACTION WITH TRAF4.
 RX PubMed=9626059;
 RA Krajewska M., Krajewski S., Zapata J.M., VanArsdale T.,
 RA Gascoyne R.D., Berern K., McFadden D., Shabaik A., Rugh J.,
 RA Reynolds A., Cleveland C.V., Reed J.C.;
 RT "TRAF-4 expression in epithelial progenitor cells. Analysis in normal
 RT adult, fetal, and tumor tissues";
 RL Am. J. Pathol. 152:1549-1561 (1998).
 RN [8]
 RP INTERACTION WITH TRAF5.
 RX MEDLINE=98172745; PubMed=9511754;
 RA Mizushima S.-I., Fujita M., Ishida T., Azuma S., Kato K., Hirai M.,
 RA Otsuka M., Yamamoto T., Inoue J.-I.;
 RT "Cloning and characterization of a cDNA encoding the human homolog of
 RT tumor necrosis factor receptor-associated factor 5 (TRAF5).";
 RL Gene 207:135-140 (1998).
 CC CC -1- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 CC LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 CC and TRAF5. May play a role in the development of lymphoid organs.
 CC CC -1- SUBUNIT: Self-associates. Associates with TRAF3, TRAF4 and TRAF5.
 CC CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC CC -1- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC -----
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@sib-sib.ch).
 CC -----
 DB EMBL; L04270; AAA36757.1; -.

STRAIN=C57BL/6; TISSUE=Kidney;
RA Isogai D., Ichino M., Yoshinari M., Yamaura A., Kurokawa F.,
RA Minami M.;
RT "Mouse DR6: mouse homolog of human TNFR-related death receptor-6
RT (DR6).";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c; TISSUE=Kidney;
RA Kim V., Machleidt T., Shi W.-X., Wang X., Cai Z.;
RA "Murine DR6: murine TNFR-related death receptor-6";
RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Kidney;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouer L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mollath S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Wozley K.C., Hale S.S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Murzyn D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krywinski M.I., Skaista U., Smalius D.E.,
RA Schnorch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [4]
RP FUNCTION.
RX MEDLINE=21571606; PubMed=11714751;
RA Zhao H., Yan M., Wang H., Erickson S., Grewal I.S., Dixit V.M.;
RT "Impaired c-Jun amino terminal kinase activity and T cell
RT differentiation in death receptor 6-deficient mice.";
RL J. Exp. Med. 194:1441-1448 (2001).
RC -!- FUNCTION: May activate NF-kappa-B and promote apoptosis (By
CC similarity). May activate JNK and be involved in T-cell
CC differentiation.
CC -!- FUNCTION: May activate NF-kappa-B and JNK and promote apoptosis.
CC May be involved in T-cell differentiation.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: Ubiquitous. Highly expressed in adult spleen,
CC thymus, testis, prostate, ovary, small intestine, colon, brain,
CC lung and kidney, and in fetal brain, liver and lung. Detected at
CC lower levels in adult peripheral blood leukocytes, lung, and in
CC fetal muscle, heart, kidney, small intestine and skin. Detected in
CC T-cells, B-cells and monocytes. In T-cells expression is highest
CC in Th0 cells, intermediate in Th2 cells and lower in Th1 cells.
CC -!- SIMILARITY: Contains 4 TNFR-Cys repeats.
CC -!- SIMILARITY: Contains 1 death domain.
CC -!- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-25 IS THE INITIATOR.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
CC or send an email to license@isb-sib.ch).
CC
CC -----
DR EMBL: AF322069; AK338115.1; -
DR EMBL: AY043489; AK741193.1; -
DR EMBL: BC016420; AAH16420.1; -
DR DDB: G014763; L120G.
DR MGD: MGI:2151075; Tnfrsf21.

DR PROSITE; PS0050; TNFR_NGFR 2; 1.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 41 POTENTIAL.
 FT CHAIN 42 655 TUMOR NECROSIS FACTOR RECEPTOR
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 42 349 SUPRAFAMILY MEMBER 21.
 FT TRANSMEM 350 370 POTENTIAL.
 FT DOMAIN 371 655 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 415 498 DEATH.
 FT REPEAT 50 88 TNFR-CYS 1.
 FT REPEAT 90 131 TNFR-CYS 2.
 FT REPEAT 133 167 TNFR-CYS 3.
 FT REPEAT 170 211 TNFR-CYS 4.
 FT DISULFID 67 80 BY SIMILARITY.
 FT DISULFID 70 88 BY SIMILARITY.
 FT DISULFID 91 106 BY SIMILARITY.
 FT DISULFID 109 123 BY SIMILARITY.
 FT DISULFID 113 131 BY SIMILARITY.
 FT DISULFID 133 144 BY SIMILARITY.
 FT DISULFID 150 168 BY SIMILARITY.
 FT DISULFID 171 186 BY SIMILARITY.
 FT DISULFID 192 211 BY SIMILARITY.
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 141 141 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 257 257 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 278 278 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 289 289 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 655 AA; 71844 MW; 48939391C4852A33 CRC64;
 Query Match 19.2%; Score 287; DB 1; Length 655;
 Best Local Similarity 34.3%; Pred. No. 58-15;
 Matches 58; Conservative 23; Mismatches 88; Indels 0; Gaps 0;
 QY 6 TYEMDAETGERLVCAQCPGTFVCRPRDSDPTTCGPPRRHYTCFMYLRCRYCNVL 65
 Db 53 YRHYDRATQVLTCKCPAGTVSEHCNTSLRVCSGCVGTFHENGIEKCHDCSQP 112
 QY 66 CGEREERARACHATNCRCTGTFPAHAGFCEHASCPCGAGVIAPGTPSQNTQCP 125
 Db 113 CFPMIEKLEPCAAITDRECTCPGFMQSNATCAPHTVCPVGVGRKGTETEDVRCKQCA 172
 QY 126 PGTFSASSSSQCPHRNCTALGALNVPGSSSHDTLCTCTGPELST 174
 Db 173 RGFSDVSSVMKRAYTDCLSCNLVWIKPGTKETDNVCGTLPSFSST 221
 RESULT 10
 ID_TNR3 MOUSE STANDARD; PRT; 415 AA.
 AC P50284;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Tumor necrosis factor receptor superfamily member 3 precursor
 DE (Lymphotoxin-beta receptor).
 GN LTER OR TNFRS3 OR TNFR.
 OS Mus musculus (mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CVB; TISSUE=Lung;
 RA MEDLINE=96072804; PubMed=7594541;
 RA Force W.R., Walter B.N., Hession C., Tizard R., Kozak C.A.,
 RA Browning J.L., Ware C.F.;
 RA "Mouse lymphotoxin-beta receptor. Molecular genetics, ligand binding,
 RT and expression.";
 RL J. Immunol. 155:5280-5288 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96163885; PubMed=8586432;

RA Nakamura T., Tashiro K., Nazarea M., Nakano T., Sasayama S.,
 RA Honjo T.;
 RA "The murine lymphotoxin-beta receptor cDNA: isolation by the signal
 RT sequence trap and chromosomal mapping.";
 RL Genomics 30:312-319 (1995).
 RN [3]
 RP INTERACTION WITH TRAF5.
 RC STRAIN=BALB/c;
 RX MEDLINE=96278943; PubMed=8663299;
 RA Nakano H., Oshima H., Chung W., Williams-Abbott L., Ware C.F.,
 RA Yagita H., Okumura K.;
 RT TRAF5, an activator of NF-kappaB and putative signal transducer for
 the lymphotoxin-beta receptor.";
 RL J. Biol. Chem. 271:14661-14664 (1996).
 CC -I- FUNCTION: Receptor for the heterotrimeric lymphotoxin containing
 LTA and LTB, and for TNFSF14/LIGHT. Promotes apoptosis via TRAF3
 and TRAF5. May play a role in the development of lymphoid organs
 (By similarity).
 CC -I- SUBUNIT: Self-associates (By similarity). Associates with TRAF5.
 CC Associates with TRAF3 and TRAF4 (By similarity).
 CC -I- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -I- SIMILARITY: Contains 4 TNFR-Cys repeats.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercia
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 or send an email to license@sib-sib.ch).
 DR EMBL; U29173; AAA68964.1; -;
 DR EMBL; L38423; AAB00846.1; -;
 DR EMBL; U30798; AAA81334.1; -;
 DR HSSP; O14763; 1D0G.
 DR MGD; MGI:104875; Ltbr.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam; PF00020; TNFR_c6; 3.
 DR SMART; SM00208; TNFR; 3.
 DR PROSITE; PS00652; TNFR_NGFR 1; 2.
 DR PROSITE; PS00505; TNFR_NGFR 2; 3.
 KW Receptor; Apoptosis; Transmembrane; Glycoprotein; Repeat; Signal.
 FT SIGNAL 1 30 POTENTIAL.
 FT CHAIN 31 415 TUMOR NECROSIS FACTOR RECEPTOR
 FT EXTRACELLULAR (POTENTIAL).
 FT DOMAIN 31 223 POTENTIAL.
 FT TRANSMEM 224 244 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 245 415 TNFR-CYS 1.
 FT REPEAT 42 81 TNFR-CYS 2.
 FT REPEAT 82 124 TNFR-CYS 3.
 FT REPEAT 125 170 TNFR-CYS 4.
 FT REPEAT 171 213 BY SIMILARITY.
 FT DISULFID 43 58 BY SIMILARITY.
 FT DISULFID 59 72 BY SIMILARITY.
 FT DISULFID 62 80 BY SIMILARITY.
 FT DISULFID 83 98 BY SIMILARITY.
 FT DISULFID 101 116 BY SIMILARITY.
 FT DISULFID 104 124 BY SIMILARITY.
 FT DISULFID 126 132 BY SIMILARITY.
 FT DISULFID 139 150 BY SIMILARITY.
 FT DISULFID 142 169 BY SIMILARITY.
 FT DISULFID 172 187 BY SIMILARITY.
 FT CARBOHYD 40 40 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 179 179 N-LINKED (GLCNAC. .) (POTENTIAL).
 SQ SEQUENCE 415 AA; 44956 MW; 29B326A56GABF661 CRC64;
 Query Match 17.8%; Score 265.5; DB 1; Length 415;
 Best Local Similarity 30.9%; Pred. No. 1.4e-13;
 Matches 72; Conservative 24; Mismatches 88; Indels 49; Gaps 10;
 QY 20 CAQCPGTFVCRPRDSDPTTCGPPRRHYTCFMYLRCRYCNVL---ERCYCNVLCGEREERARAC 76
 Db 59 CSRCPGTFVCRPRDSDPTTCGPPRRHYTCFMYLRCRYCNVLCGEREERARAC 116

```

QY 77 HATHNRACRCRTGTFEFAHAGFCL-----EHASCPPGAGVIA-PGTPSQNT-----QCQP 123
Db 117 TSDRKAECRCQPGM-----SCVYLNCEVHCERLVLCPGTEAEVTDIEMDIDVNCVP 171
QY 124 CPPTTFSSSSSSQCPHNCIHLGALNVPGSSSHDTLTCTGTFPLSTFVPGARECE 183
Db 172 CKPHQNTSPRARCQPHTRCE-QGIVEAAPGTSYDTICK-----NPPFEGAMLL 224
QY 184 RAVIDFVAF-----QDISIKRLQRLQALEAPEGWS-----PTPRA 219
Db 225 ALLSLVLFLETTVLACANRHSHSLCKLGLTLK--RHPGESESPCPAPRA 275

RESULT 11
CRMB VARV STANDARD; PRT; 349 AA.
AC P34015; Q85407; Q83098; Q891118;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Soluble TNF receptor II precursor (cytokine response modifying protein
DE B).
DE CRMS OR G2R OR G4R.
OS Variola virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10253;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=India-1967 / Isolate Ind3;
RX MEDLINE=93202281; PubMed=8384129;
RA Shchelkunov S.N., Blinov V.M., Sandakhchiev L.S.;
RT "Genes of variola and vaccinia viruses necessary to overcome the host
RL protective mechanisms.";
RN FEBS Lett. 319:80-83(1993).
RP SEQUENCE FROM N.A.
RC STRAIN=Bargladesh-1975;
RX MEDLINE=94088747; PubMed=8264798;
RA Massung J.F., Esposito J.J., Liu L., Qi J., Utterback T.R.,
RA Knight J.C., Aubin L., Yuran T.E., Parsons J.M., Loparev V.N.,
RA Salivanov N.A., Cavallaro K.F., Kerlavage A.R., Mahy B.W.J.,
RA Venter C.J.;
RT "Potential virulence determinants in terminal regions of variola
RT smallpox virus genome.";
RL Nature 366:748-751(1993).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Garcia-1966, and Somalia-1977;
RA Massung J.F., Loparev V.N., Knight J.C., Chizhikov V.E., Parsons J.M.,
RA Totmenin A.V., Shchelkunov S.N., Esposito J.J.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=Garcia-1966;
RX MEDLINE=20107289; PubMed=10639322;
RA Shchelkunov S.N., Totmenin A.V., Loparev V.N., Safronov P.F.,
RA Gutorov V.V., Chizhikov V.E., Knight J.C., Parsons J.M., Massung R.F.,
RA Esposito J.J.;
RT "Astrim smallpox variola minor virus genome DNA sequences.";
RL Virology 266:361-386(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=Butler-1952, Chimp 9-4, Garcia-1966, and Somalia-1977;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species.";
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to
CC the modification of TNF-mediated antiviral processes (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

```

```

CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement. See http://www.isb-sib.ch/announce/
CC or send an email to license@sb-sib.ch).
CC -----
CC EMBL; X69198; CAA49137.1; -
CC EMBL; X61117; CAA47540.1; -
CC EMBL; L22579; AAA60933.1; -
CC EMBL; U18339; AAA69407.1; -
CC EMBL; U18341; AAA69467.1; -
CC EMBL; Y16780; CAB54798.1; -
CC EMBL; U88146; AAB94371.1; -
CC EMBL; U88148; AAB94373.1; -
CC EMBL; U88149; AAB94374.1; -
CC EMBL; U88152; AAB94377.1; -
CC PIR; D36858; D36858.
CC PIR; D72175; D72175.
CC PIR; T28623; T28623.
CC HSPF; O14763; LDOG.
CC InterPro; IPR001368; TNFR_C6.
CC Pfam; PF00020; TNFR_C6; 2.
CC SMART; SM00208; TNFR; 3.
CC PROSITE; PS00652; TNFR_NGFR_1; 2.
CC PROSITE; PS00500; TNFR_NGFR_2; 2.
CC Receptor; Glycoprotein; Repeat; Signal.
KW SIGNAL 1 22
FT CHAIN 23 349 SOLUBLE TNF RECEPTOR II.
FT REPEAT 31 66 TNFR-CYS 1.
FT REPEAT 67 108 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 65 BY SIMILARITY.
FT DISULFID 68 83 BY SIMILARITY.
FT DISULFID 86 100 BY SIMILARITY.
FT DISULFID 90 108 BY SIMILARITY.
FT CARBOHYD 101 101 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 173 173 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 215 215 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 248 248 N-LINKED (GLCNAC. .) (POTENTIAL).
FT VARIANT 17 17 MISSING (IN STRAINS BANGLADESH-1975 AND
FT VARIANT 160 160 CHIMP 9-4).
FT VARIANT 165 165 H -> Y (IN STRAINS BUTLER-1952, GARCIA-
FT VARIANT 182 182 1966 AND SOMALIA-1977).
FT VARIANT 274 274 A -> T (IN STRAINS BUTLER-1952 AND
FT VARIANT 335 335 GARCIA-1966).
FT VARIANT 339 339 E -> K (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 A -> E (IN STRAIN SOMALIA-1977).
FT VARIANT 339 339 N -> D (IN STRAINS BUTLER-1952 AND
FT SEQUENCE 349 AA; 38189 MM; D45D40B5C6E780EF CRC64;
Query Match 17.4%; Score 260; DB 1; Length 349;
Best Local Similarity 32.2%; Pred. No. 3, 1e-13;
Matches 59; Conservative 26; Mismatches 90; Indels 8; Gaps 3;
QY 5 PTYPMRDAE-TGERLVCAQCPGTFVQVPCRRDSTTCGPPCPRHVYTFMNYLCRYCN 63
Db 28 PNGKCKDTEYKRNLCCLCPGTFVASRLCDSKNTQCTPGSGTFTSRNNHLPACLSCN 87
QY 64 VLQGEREEARACHATHNRCRCRTGFF-----AHAGFCLEHASCPPGAGVIACTPSQ 117
Db 88 GRCSNQVETSCNTNTRICECSPGYCLLKGSSGCKACVCSQTKCGIGYGV-SGHTSWG 146
QY 118 NTQCQPCPPGTFSSASSSEOCQHRNCTALGLALNVPGSSSHDTLTCTGTFPLSTFV 177

```

Db 147 DVICSPGFGYSHYTVSSADKCEPVNTNFYIDVEITLYPVNDTSCTRTTIGLSISIL 206

QY 178 GAE 180

Db 237 TSE 209

RESULT 2

CRMS CAMPS

ID CRMB CAMPS STANDARD; PRT; 349 AA.

AC Q8UYA7;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Soluble TNF receptor II precursor [cytokine response modifying protein B].

DE (CRMB1 OR CMP2L OR CMLV002) AND (CRMB2 OR CMP205R OR CMLV210).

GN Camelpox virus [strain CMS], and

OS Camelpox virus [strain M-96].

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=203172, 203173;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CMS;

RX PubMed=11907336;

RA Gubser C., Smith G.J.;

RT "The sequence of camelpox virus shows it is most closely related to variola virus, the cause of smallpox.";

RT J. Gen. Virol. 83:855-872(2002).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=M-96;

RA Alfonso C.L., Tulman E.R., Lu Z., Zsak L., Zaitsev V.L., Kerembekova U.Z., Sandybaev N.T., Kutish G.F., Rock D.L.;

RT "The genome of camelpox virus.";

RL Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes (By similarity).

CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).

CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; AY009089; AAG37456.1; -

DR EMBL; AY009089; AAG37718.1; -

DR EMBL; AF438165; AAL73920.1; -

DR EMBL; AF438165; AAL73917.1; -

DR InterPro; IPR001368; TNFR_C6.

DR Pfam; PF00020; TNFR_C6; 2.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS00650; TNFR_NGFR_2; 2.

KW Receptor; Glycoprotein; Repeat; Signal.

FT SIGNAL 1 19 POTENTIAL.

FT CHAIN 20 349 SOLUBLE TNF RECEPTOR II.

FT REPEAT 31 65 TNFR-CYS 1.

FT REPEAT 67 108 TNFR-CYS 2.

FT DISULFID 32 43 BY SIMILARITY.

FT DISULFID 44 57 BY SIMILARITY.

FT DISULFID 47 65 BY SIMILARITY.

FT DISULFID 68 83 BY SIMILARITY.

FT DISULFID 86 100 BY SIMILARITY.

FT DISULFID 90 108 BY SIMILARITY.

FT CARBOHYD 101 101 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 189 189 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 248 248 N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 349 AA; 38064 MW; EA412AF991E087F3 CRC64;

Query Match 17.3%; Score 257.5; DB 1; Length 349;

Best Local Similarity 32.0%; Pred. No. 4.9e-13;

Matches 54; Conservative 28; Mismatches 80; Indels 7; Gaps 2;

QY 18 LVCAQCPFGTFVORPCRRDSPTTCGPPRHRYTQFMNLYLCRYCNVLCGEREEERACH 77

Db 42 LCCLSCPFGTVASRLCDSKINTQCTPCGSGTFTSRNNHLPACLSNCRCDQSNQVETRSCN 101

QY 78 ATHNACRCRTGFF-----AHAGCLEHASCPGAGVIAPGTFPSONTQCPCPPTFSA 131

Db 102 TTHNRICRSPGYCYLKGSSGCKACVSGTKGIGYGV--SGHTSAGDVICSPGGLGYTSR 160

QY 132 SSSSESQCPHRNCTALGALNVPGSSSHDTLCTCTGFPPLSTRVPGA 180

Db 161 TVSSADKCEPVPSNTFNYIDVEINLYPVNDTSCTRTTIGISISTSE 209

RESULT 13

CRMB COMPEX

ID CRMB COMPEX STANDARD; PRT; 351 AA.

AC Q73559;

DT 28-FEB-2003 (Rel. 41, Created)

DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 28-FEB-2003 (Rel. 41, Last annotation update)

DE Soluble TNF receptor II precursor (cytokine response modifying protein B).

DE (CRMB1 OR D2L) AND (CRMB2 OR H4R).

OS Cowpox virus (CPV).

OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;

OC Orthopoxvirus.

OX NCBI_TaxID=10243;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=GRI-90 / Grishak;

RX MEDLINE=98229462; PubMed=9568042;

RA Shchelkunov S.N., Safonov P.F., Totmenin A.V., Petrov N.A., Ryazankina O.I., Gutorov V.V., Kotwal G.J.;

RT "The genomic sequence analysis of the left and right species-specific terminal region of a cowpox virus strain reveals unique sequences and a cluster of intact ORFs for immunomodulatory and host range proteins.";

RT Virology 243:432-460(1998).

RL [2]

RP FUNCTION.

RC STRAIN=Brighton red;

RX MEDLINE=94378510; PubMed=8091655;

RA Hu F.Q., Smith C.A., Pickup D.J.;

RT "Cowpox virus contains two copies of an early gene encoding a soluble secreted form of the type II TNF receptor.";

RL Virology 204:343-356(1994).

CC -!- FUNCTION: Receptor for TNF-alpha and TNF-beta. May contribute to the modification of TNF-mediated antiviral processes.

CC -!- SUBCELLULAR LOCATION: Secreted.

CC -!- SIMILARITY: Contains 2 TNFR-Cys repeats.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).

DR EMBL; Y11842; CAA72578.1; -

DR EMBL; Y15035; CAA75306.1; -

DR HSSP; O14763; ID03.

DR InterPro; IPR001368; TNFR_C6.

DR Pfam; PF00020; TNFR_C6; 2.

DR SMART; SM00208; TNFR; 3.

DR PROSITE; PS00652; TNFR_NGFR_1; 2.

DR PROSITE; PS00500; TNFR_NGFR 2; 2.
KW Receptor; Glycoprotein; Repeat; Signal.
FT SIGNAL 1 19 POTENTIAL.
FT CHAIN 20 351 SOLUBLE TNF RECEPTOR II.
FT REPEAT 31 67 TNFR-CYS 1.
FT REPEAT 69 110 TNFR-CYS 2.
FT DISULFID 32 43 BY SIMILARITY.
FT DISULFID 44 57 BY SIMILARITY.
FT DISULFID 47 67 BY SIMILARITY.
FT DISULFID 70 85 BY SIMILARITY.
FT DISULFID 88 102 BY SIMILARITY.
FT DISULFID 92 110 BY SIMILARITY.
FT CARBOHYD 103 103 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 351 AA; 38253 MW; 57CAE73EF4E5D7C7 CRC64;
Query Match 17.1%; Score 254.5; DB 1; Length 351;
Best Local Similarity 32.2%; Pred. NO. 8.4e-13;
Matches 55; Conservative 29; Mismatches 78; Indels 9; Gaps 3;
Qy 18 LVCAQCPTGVORPC--RRDSPTTCGPPRRHYTQFWNYLERCKRYCNVLCGEREEHARA 75
Db 42 LCCLSCPPTVASRLCDKSTNTNQTCTPGSGTFSRNHLPACLSNGRCDSNQVETR 101
Qy 76 CHATHNACRCRTGFF-----AHAGFCLEHACPPGAGVIAPGTPSNTQCPGPGTF 129
Db 102 CYNTHNICECAPGYICLLKSSGCKACVSQTKGIGYGV-SGHTSTGDDVWCSPGLGT 160
Qy 130 SASSSSQCPHRCNTALGALNVPGSSSDHTLCTCTGPFPLTRVPGAE 180
Db 161 SHTVSSADKCEPVSNFNTNYIDWEINLPVNDTCTRTTTGLSEISTSE 211
RESULT 14
TR14 HUMAN STANDARD; PRT; 283 AA.
AC Q92956; Q8WXR1; Q96J31; Q9UM65;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 14 precursor
DE (Herpesvirus entry mediator A) [Tumor necrosis factor receptor-like 2]
DE (TR2)
GN TNFRSF14 OR HVEM OR HVEM-1
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
FP SEQUENCE FROM N.A.
RC TISSUE=Cervical adenocarcinoma;
RX MEDLINE=97053782; PubMed=8898196;
RA Montgomery R.I., Warner M.S., Lum B.J., Spear P.G.;
RT "Herpes simplex virus-1 entry into cells mediated by a novel member of
RL the TNF/NGF receptor family.";
RN Cell 87:427-436(1996).
[2]
FP SEQUENCE FROM N.A.
RX MEDLINE=97306336; PubMed=9162061;
RA Kwon B.S., Tan K.B., Ni J., Oh K.-O., Lee Z.H., Kim K.K., Kim Y.-J.,
RA Wang S., Gentz R., Yu G.-L., Harrop J., Lyn S.D., Silverman C.,
RA Porter T.G., Truneh A., Young P.R.;
RT "A newly identified member of the tumor necrosis factor receptor
RL superfamily with a wide tissue distribution and involvement in
RN lymphocyte activation.";
RN J. Biol. Chem. 272:14272-14276(1997).
[3]
FP SEQUENCE FROM N.A.
RX Zhang W., Wan T., Cao X.;
RA Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
[4]
FP SEQUENCE FROM N.A., AND VARIANTS ARG-17 AND ILE-241.

RX MEDLINE=21629477; PubMed=11756979;
RA Struyf F., Posavac C.M., Keyaerts E., Van Ranst M., Corey L.,
RA Spear P.G.;
RT "Search for polymorphisms in the genes for herpesvirus entry mediator,
RT Nectin-1, and Nectin-2 in immune seronegative individuals.";
RL J. Infect. Dis. 185:36-44(2002).
[5]
RN SEQUENCE FROM N.A.
RC TISSUE=Skin;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smalios D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RL human and mouse cDNA sequences.";
RN Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[6]
FP INTERACTION WITH TRAF2 AND TRAF5.
RX PubMed=9153189;
RA Hsu H., Solovvey I., Colombero A., Elliott R., Kelley M., Boyle W.J.;
RT "ATAR, a novel tumor necrosis factor receptor family member, signals
RT through TRAF2 and TRAF5.";
RL J. Biol. Chem. 272:13471-13474(1997).
[7]
FP INTERACTION WITH TRAF3 AND TRAF5.
RX PubMed=9162022;
RA Marsters S.A., Ayres T.M., Skubatch M., Gray C.L., Rothe M.,
RA Ashkenazi A.;
RT "Herpesvirus entry mediator, a member of the tumor necrosis factor
RT receptor (TNFR) family, interacts with members of the TNFR-associated
RT factor family and activates the transcription factors NF-kappaB and
RT AP-1.";
RN J. Biol. Chem. 272:14029-14032(1997).
[8]
FP X-RAY CRYSTALLOGRAPHY (2.65 ANGSTROMS) OF 39-200.
RX MEDLINE=21403268; PubMed=11511370;
RA Carfi A., Willis S.H., Whitbeck J.C., Krumenacher C., Cohen G.H.,
RA Eisenberg R.J., Wiley D.C.;
RT "Herpes simplex virus glycoprotein D bound to the human receptor
RL HveA".
RN Mol. Cell 8:169-179(2001).
CC -!- FUNCTION: Receptor for TNFSF14/LIGHT and homotrimeric
CC TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays
CC an important role in HSV pathogenesis because it enhanced the
CC entry of several wildtype HSV strains of both serotypes into CHO
CC cells, and mediated HSV entry into activated human T cells.
CC -!- SUBUNIT: INTERACTS WITH TRAF2, TRAF3 AND TRAF5.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Probable).
CC -!- TISSUE SPECIFICITY: WIDELY EXPRESSED, WITH THE HIGHEST EXPRESSION
CC IN LUNG, SPLEEN, AND THYMUS.
CC -!- SIMILARITY: Contains 3 TNFR-Cys repeats.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).


```
CC BMBL; U7C321; AAB58354.1; --
DR DBL; U81232; AAD00505.1; --
DR EMBL; AF153978; AAF7588.1; --
DR EMBL; AF373877; AAL47717.1; --
DR EMBL; AF373878; AAL47718.1; --
DR EMBL; BC002794; AAH02794.1; --
DR PDB; 1JWA; 26-SEP-01.
DR Genew; HGNC:11912; TNFRSF14.
DR MIX; 602746; --
DR GO; GO:0005027; F-NGF/TNF (6 C-domain) receptor activity; TAS.
DR GO; GO:0007166; P-cell surface receptor linked signal transdu. .; TAS.
DR GO; GO:0006955; P-immune response; TAS.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 3.
DR SMART; SM00208; TNFR; 3.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00650; TNFR_NGFR_2; 2.
DR Receptor; Transmembrane; Glycoprotein; Repeat; Signal; Polymorphism;
KW 3D-structure.
FT SIGNAL 1 38
FT CHAIN 39 233
FT FT FT
FT DOMAIN 39 222
FT TRANSMEM 203 223
FT DOMAIN 224 283
FT REPEAT 42 75
FT REPEAT 78 119
FT REPEAT 121 162
FT DISULFID 42 53
FT DISULFID 54 67
FT DISULFID 57 75
FT DISULFID 78 93
FT DISULFID 96 111
FT DISULFID 99 119
FT DISULFID 121 138
FT DISULFID 127 135
FT CARBOHYD 110 110
FT CARBOHYD 173 173
FT VARIANT 17 17
FT VARIANT 241 241
FT TURN 44 45
FT STRAND 46 46
FT STRAND 49 49
FT TURN 50 51
FT STRAND 52 52
FT STRAND 55 55
FT STRAND 57 57
FT TURN 59 60
FT STRAND 61 61
FT STRAND 74 77
FT TURN 80 81
FT STRAND 82 83
FT STRAND 88 88
FT STRAND 94 95
FT TURN 101 104
FT STRAND 105 109
FT STRAND 118 121
FT TURN 123 124
FT STRAND 125 129
FT STRAND 137 140
SQ SEQUENCE 283 AA; 30392 MW; 46CE13C2C70242C1 CRC64;
Query Match 16.4%; Score 244; DB 1; Length 283;
Best Local Similarity 37.3%; Pred. No. 4.3e-12;
Matches 56; Conservative 14; Mismatches 68; Indels 12; Gaps 4;
QY 20 CAQCPPTGVQPCRRDSPTTCGPPRHYYTGFNYLER---CRYCNVLGGRREBEARAC 76
DB 54 CPKCSPGYRVKREACGELGTGTCVPCPPGGTYIAHLNGLSKLCCQWCDPMGLR--ASRNC 111
```

```
QY 77 HATHNACRCRTGFFA-----HAGFCLSEASCPPGAGVIAPTFPSQNTQCQCPPTGTF 130
DB 112 SRTEAVCGSPGHFCIVQGDHCAACRAYATSPGQVOKGTESQDTLCQNCPPGTF 171
QY 131 ASSSSSECCOPHNCNTALGLALNVPGSSSH 160
DB 172 -PNGTLEECQHQTKCSWLVTKAGAGTSSSH 200

RESULT 15
TR11 HUMAN
ID TR11 HUMAN STANDARD; PRT; 616 AA.
AC Q9Y6G6;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Tumor necrosis factor receptor superfamily member 11A precursor
DE (Receptor activator of NF-kappaB) (Osteoclast differentiation factor
DE receptor) (ODFR).
DE TNFRSF11A OR RANK.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dendritic cell;
RX MEDLINE=98032977; PubMed=9367155;
RA Anderson D.M., Maraskovsky E., Billingsley W.L., Dougall W.C.,
RA Tometsko M.E., Roux E.R., Teepe M.C., DuBose R.F., Cosman D.,
RA Galibert L.;
RT "A homologue of the TNF receptor and its ligand enhance T-cell growth
RT and dendritic-cell function."
RL Nature 390:175-179 (1997).
RN [2]
RP FUNCTION.
RX MEDLINE=99097247; PubMed=9878548;
RA Nakagawa N., Kinoshita M., Yamaguchi K., Shima N., Yasuda H., Yano K.,
RA Morinaga T., Higashio K.;
RT "RANK is the essential signaling receptor for osteoclast
RT differentiation factor in osteoclastogenesis."
RL Biochem. Biophys. Res. Commun. 253:395-400 (1998).
RN [3]
RP INTERACTION WITH TRAF1; TRAF2; TRAF3; TRAF5 AND TRAF6.
RX PubMed=9774460;
RA Wong B.R., Josien R., Lee S.Y., Volodgoda M., Steinman R.M.,
RA Choi Y.;
RT "The TRAF family of signal transducers mediates NF-kappaB activation
RT by the TRANCE receptor."
RL J. Biol. Chem. 273:28355-28359 (1998).
RN [4]
RP VARIANT FEO 16-LEU--LEU-21 DUPL, VARIANT PDB2 13-ALA--LEU-21 DUPL, AND
RP VARIANT VAL-192.
RX MEDLINE=20082806; PubMed=10615125;
RA Hughes A.E., Ralston S.H., Marken J., Bell C., MacPherson H.,
RA Wallace R.G.H., van Hul W., Whyte M.P., Nakatsuka K., Hovy L.,
RA Anderson D.M.;
RT "Mutations in TNFRSF11A, affecting the signal peptide of RANK, cause
RT familial expansile osteolysis."
RL Nat. Genet. 24:45-48 (2000).
CC -!- FUNCTION: Receptor for TNFRSF11/RANKL/TRANCE/OPGL; essential for
CC RANKL-mediated osteoclastogenesis. Involved in the regulation of
CC interactions between T-cells and dendritic cells.
CC -!- SUBUNIT: Interacts with TRAF1, TRAF2, TRAF3, TRAF5 and TRAF6.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -!- TISSUE SPECIFICITY: UBQUITOUS EXPRESSION WITH HIGH LEVELS IN
CC SKELETAL MUSCLE, THYMUS, LIVER, COLON, SMALL INTESTINE AND ADRENAL
CC GLAND.
CC -!- DISEASE: DEFECTS IN TNFRSF11 ARE THE CAUSE OF FAMILIAL EXPANSILE
CC OSTEOLYSIS (FEO), A RARE AUTOSOMAL DOMINANT BONE DISORDER
CC CHARACTERIZED BY FOCAL AREAS OF INCREASED BONE REMODELLING. THE
CC OSTEOLYTIC LESIONS DEVELOP USUALLY IN THE LONG BONES DURING EARLY
CC ADULTHOOD. FEO IS OFTEN ASSOCIATED WITH EARLY ONSET DEAFNESS AND
```


GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 3, 2003, 13:08:01 ; Search time 41 Seconds
(without alignments)
1705.665 Million cell updates/sec

Title: US-10-069-385-1
Perfect score: 1491
Sequence: 1 VAETPTPWRDAETGRLVC.....RVAMPGLSVRRLPLVH 271

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SPTREMBL 23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phase:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp Vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriap:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	499.5	33.5	285	13 Q90W71	Q90W71 oncorhynch
2	486.5	32.6	285	13 Q90YS6	Q90YS6 oncorhynch
3	395	26.5	302	13 Q9PJ50	Q9PJ50 salvelinus
4	333.5	22.4	459	11 Q62327	Q62327 mus musculus
5	327	21.9	482	11 Q88734	Q88734 mus musculus
6	317.5	21.3	457	4 Q8IVS6	Q8IVS6 homo sapien
7	313.5	21.0	433	11 Q9IZM6	Q9IZM6 rattus norv
8	287	19.2	651	13 Q98SM6	Q98SM6 gallus gall
9	275	18.4	348	12 Q57108	Q57108 monkeypox v
10	275	18.4	348	12 Q57277	Q57277 monkeypox v
11	275	18.4	348	12 Q57103	Q57103 monkeypox v
12	270.5	18.1	349	12 Q57100	Q57100 monkeypox v
13	268.5	18.0	349	12 Q57101	Q57101 monkeypox v
14	268.5	18.0	349	12 Q57102	Q57102 monkeypox v
15	268.5	18.0	349	12 Q57291	Q57291 monkeypox v
16	267.5	17.9	349	12 Q57099	Q57099 monkeypox v

17	260	17.4	348	12	Q57112	Q57112 variola vir
18	260	17.4	349	12	Q57111	Q57111 variola vir
19	260	17.4	349	12	Q57110	Q57110 variola vir
20	260	17.4	350	12	Q57116	Q57116 cowpox viru
21	259	17.4	360	12	Q57118	Q57118 cowpox viru
22	258.5	17.3	355	12	Q85308	Q85308 cowpox viru
23	257.5	17.3	326	12	Q57120	Q57120 cowpox viru
24	257.5	17.3	349	12	Q57098	Q57098 camelpox vi
25	257.5	17.3	349	12	Q57284	Q57284 camelpox vi
26	254.5	17.1	326	12	Q57122	Q57122 cowpox viru
27	253.5	17.0	349	12	Q57097	Q57097 camelpox vi
28	253.5	17.0	349	12	Q57305	Q57305 cowpox viru
29	253.5	17.0	351	12	Q57117	Q57117 cowpox viru
30	252	16.9	349	12	Q57109	Q57109 variola vir
31	251	16.8	347	12	Q57119	Q57119 cowpox viru
32	249.5	16.7	347	12	Q57115	Q57115 cowpox viru
33	248.5	16.7	351	12	Q57121	Q57121 cowpox viru
34	245.5	16.5	350	12	Q57123	Q57123 cowpox viru
35	244	16.4	283	6	Q9XS28	Q9XS28 cercopithec
36	230.5	15.5	276	13	Q9DDDD2	Q9DDDD2 gallus gall
37	227	15.2	278	6	Q8SQ34	Q8SQ34 sus scrofa
38	224	15.0	573	11	Q8BZU6	Q8BZU6 mus musculu
39	219.5	14.7	277	6	Q8WMO2	Q8WMO2 ovis aries
40	203.5	13.6	267	6	Q02764	Q02764 oryctolagus
41	203	13.6	289	11	Q8K2X6	Q8K2X6 mus musculu
42	202	13.5	132	13	Q90T18	Q90T18 salvelinus
43	200	13.4	167	12	Q9DUL2	Q9DUL2 cowpox viru
44	200	13.4	169	11	Q9JKE0	Q9JKE0 rattus norv
45	199	13.3	167	12	Q8UYL3	Q8UYL3 vaccinia vi

ALIGNMENTS

RESULT 1

Q90W71	ID	Q90W71	PRELIMINARY;	PRT;	285 AA.
AC	Q90W71;				
DT	01-DEC-2001	(TREMBLrel. 19, Created)			
DT	01-DEC-2001	(TREMBLrel. 19, last sequence update)			
DT	01-MAR-2003	(TREMBLrel. 23, last annotation update)			
DE	Putative decoy receptor 3 protein.				
OS	Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Actinopterygii; Neopterygii; Teleostei; Euteleostei;				
OC	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.				
OX	NCBI_TaxID=8022;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Leukocyte;				
RA	Pleguezuelos C.; Secombes C.J.;				
RT	"Screening a rainbow trout (Oncorhynchus mykiss) cDNA library."				
RL	Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.				
DR	EMBL;	AJ315137;	CAC43329.1;	-	
DR	InterPro;	IPR006209;	EGF like.		
DR	InterPro;	IPR001368;	TNFR_c6.		
DR	Pfam;	PF00020;	TNFR_c6;	3.	
DR	SMART;	SM00208;	TNFR;	3.	
DR	PROSITE;	PS01186;	EGF 2;	1.	
DR	PROSITE;	PS00652;	TNFR_NGFR_1;	1.	
DR	PROSITE;	PS50050;	TNFR_NGFR_2;	1.	
KW	Receptor.				
SQ	SEQUENCE 285 AA; 31642 MM; FB7SCFFCIEJ91AD0 CRC64;				

Query Match 33.5%; Score 499.5; DB 13; Length 285;

Best Local Similarity 37.1%; Pred. No. 1.3e-36;

Matches 99; Conservative 41; Mismatches 116; Indels 11; Gaps 4;

QY 2 AETPTPWRDAETGRLVCACQPGTFVQRPCKRDSPTTCGCPPHRYTFWNLBRCY 61

Db 26 AHTPTYWRDDATGDSLTCDLCAPGYLLKHCTKDRKSDCGPCPKSHYTIWNYIERQY 85

QY 62 CNVLGGEREEARACHATNTRACRCCTGTGFAHAGFCLEHASCPFGAGVIAPGPSQNTQC 121

Db 86 CNRFTADEIESVPTCTQHNRCQCKGFGYTHGSCSRHRCPPGEGVINSNGTAHTDYKC 145
 QY 122 QPCPPGTFSSASSSECCQPHRNTCTALGLALNVPGSSSHDILCTCTGTFPLSTRVPGABE 181
 Db 146 EPCVPGFSSAVSSSRKACQKFSVCPGG--ITIFGNDMDVYCSACTNG--SRTHEGSAI 201
 QY 182 CERAVIDFVAQDISIKRLQLQALEAPEGCGTPPRAGRAALQKLRRLTELLGAGDG 241
 Db 202 CDGSEMEFLSLQITPRKDKELVAVLRSSAGKATT---NNATVLDLLKTIKNKAGKH-- 255
 QY 242 ALLVRLQLALRVARMGGLERSVRRFL 268
 Db 256 -FAIQMRDILNTDRLHLRTKVNKWL 281

RESULT 2

Q90YS6
 ID Q90YS6 PRELIMINARY; PRT; 285 AA.
 AC Q90YS6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE TNF decoy receptor.
 OS Oncorhynchus mykiss (Rainbow trout) (Salmo gairdneri).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Liu L., Fujiki K., Dixon B., Sundick R.S.;
 RT "Cloning of a novel rainbow trout (Oncorhynchus mykiss) CC chemokine
 RT with a fractalkine-like stalk and a TNF decoy receptor using cDNA
 RT fragments containing AU-rich elements."
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF401631; AAX91758.1;
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 3.
 DR SMART: SM00208; TNFR; 3.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 285 AA; 31795 MW; 5E3BD1B6EFC6BABC CRC64;

Query Match 32.6%; Score 486.5; DB 13; Length 285;
 Best Local Similarity 36.3%; Pred. No. 1.9e-35;
 Matches 97; Conservative 41; Mismatches 118; Indels 11; Gaps 4;
 QY 2 AETPTFWDAETGERLYCAQCPTGVQVRCRRDSPTTCGCPPRHYTQFWNYLERCRY 61
 Db 26 AHTPTIWRDADGSLTCDLCAPGTILKHTCDKRSDCGCPKSHYTEIWNVIERCQY 85
 QY 62 CNVLGGEREERACHATHNRACRTGFFAHAGFLEHASCPPGAGVIAPGTPSNTQOC 121
 Db 86 CNRFTADEIESVPTCTQHNRCQCKGFGYTHGSCSRHRCPPGEGVINSNGTAHTDYKC 145
 QY 122 QPCPPGTFSSASSSECCQPHRNTCTALGLALNVPGSSSHDILCTCTGTFPLSTRVPGABE 181
 Db 146 EPCVPGFSSAVSSSRKACQKFSVCPG--GRITIFGNDMDVYCSACRNG--SRTHEGSAI 201
 QY 182 CERAVIDFVAQDISIKRLQLQALEAPEGCGTPPRAGRAALQKLRRLTELLGAGDG 241
 Db 202 CDGSEMEFLSLQITPRKDKELVAVLRSSAGKATT---NNATVLDLLKTIKNKAGKH-- 255
 QY 242 ALLVRLQLALRVARMGGLERSVRRFL 268
 Db 256 -FAIQMRDILNTDRLHLRTKVNKWL 281

RESULT 3

Q9PUS0
 ID Q9PUS0 PRELIMINARY; PRT; 302 AA.
 AC Q9PUS0;
 DT 01-MAY-2003 (TrEMBLrel. 13, Created)
 DT 01-MAY-2003 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Decoy TNF receptor.
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OX NCBI_TaxID=8038;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bobe J., Goetz F.W.;
 RT "A tumor necrosis factor decoy receptor homologue is up-regulated in
 RT the brook trout (Salvelinus fontinalis) ovary at the completion of
 RT ovulation."
 RL Biol. Reprod. 62:420-426 (2000).
 DR EMBL: AF156738; AAD56428.1; -.
 DR HSSP: O14763; 1D4V.
 DR InterPro: IPR006209; EGF like.
 DR InterPro: IPR001368; TNFR_c6.
 DR Pfam: PF00020; TNFR_c6; 4.
 DR SMART: SM00208; TNFR; 4.
 DR PROSITE: PS01186; EGF_2; 1.
 DR PROSITE: PS00652; TNFR_NGFR_1; 1.
 DR PROSITE: PS50050; TNFR_NGFR_2; 1.
 KW Receptor.
 SQ SEQUENCE 302 AA; 34037 MW; B44C73477F05C3DF CRC64;
 Query Match 26.5%; Score 395; DB 13; Length 302;
 Best Local Similarity 34.3%; Pred. No. 2.8e-27;
 Matches 82; Conservative 44; Mismatches 101; Indels 12; Gaps 7;
 QY 6 TYPWRDAETGERLYCAQCPTGVQVRCRRDSPTTCGCPPRHYTQFWNYLERCRYCNVL 65
 Db 22 TFKNDERYSGLSIVCDRCPPGTILRAPCSANRKSQCAECPNGAYTEFWNHISKLRCS-W 80
 QY 66 CGEEREERACHATHNRACRTGFFAHAGF--CLEHASCPPGAGVIAPGTPSNTQOCQ 123
 Db 81 CAENQVYKQECSPNNCECECKEGYFNKKYACIKKKECPGYGANTTGPHTQTECVQ 140
 QY 124 CPGTTFSSASSSECCQPHRNTCTALGLALNVPGSSSHDILCTCTGTFPLSTRVPGABE 183
 Db 141 CQAGFYSEVSSAKATCLAQSNCKYGGLRVVLKGGQDWHNTLCASC--YDKTR-DGAEXLH 197
 QY 184 RAVIDFV--AFQDISIKRLQLQALEAPEGCGTPPRAGRAALQKLRRLTELLGAGD 240
 Db 198 EILPTFFIQLHTQVGIKWRRL--AMRLPQGGGKKELIG--AVMKRNRRLHDFMNSWD 252
 RESULT 4
 Q62327
 ID Q62327 PRELIMINARY; PRT; 459 AA.
 AC Q62327;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Murine tumour necrosis factor receptor 2 protein (Fragment).
 GN TNFRSF1B.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NOD;
 RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
 RT "Amino acid variation in the tumor Necrosis factor receptor 2 is
 RT linked to autoimmune diabetes in NOD mice."
 RL Genomics 0:0-0(0).

```

RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MOD;
RX MEDLINE=95178948; PubMed=7873884;
RA Powell E.E., Wicker L.S., Peterson L.B., Todd J.A.;
RT "Allelic variation of the type 2 tumor necrosis factor receptor
  gene.";
RL Mamm. Genome 5:726-727(1994).
DR EMBL; X76401; CAA53981.1; -.
DR HSSP; P19438; INCF.
DR MGD; MGI:1314883; Tnfrsf1b.
DR InterPro; IPR001368; TNFR_C6.
DR SMART; SM00208; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 1
FT VARIANT 87 87 S -> T.
FT VARIANT 93 93 T -> I.
FT VARIANT 268 268 F -> I.
FT VARIANT 345 345 S -> F.
FT VARIANT 421 421 Y -> C.
SQ SEQUENCE 459 AA; 48686 MW; 6C51D2CF1C4626DF CRC64;

Query Match 22.4%; Score 333.5; DB 11; Length 459;
Best Local Similarity 29.7%; Pred. No. 1.3e-21;
Matches 81; Conservative 43; Mismatches 110; Indels 39; Gaps 9;

QY 17 RVLCACCPGTFVQPCRRDPTTCGPPRHVYTFWNYLCRYCNVLCGRERARAC 76
DB 37 QMCCAKCPGQVKGFCNKTSDTVCADCEASMYTQVWNOFRITCLSCSSCSTDQVET 96
QY 77 HATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPTGPPSNTQCP 129
DB 97 TKQNVKVCACEAGRYCALKTHSGSCRCQKRLSKCGFGVASSRAFNNGVNLCK 156
QY 130 SASSSSSQCPHRCNTALGLALNVPGSSSHDTLCCT----SCTGFPLSTRVPG 185
DB 157 SDTTSSTVCRPHRICSIILA----IPGNASTDAVCAPESTLSAIPRTLYVSG 212
QY 186 VDFVAFQD-SIKRLQRLQALEAPGEGMPTP-----RAGRAALQKLRLRLT 240
DB 213 FLD-----QEPGSPQPSILTSI-----GSTPIEQSTKGGISLPIGLIVG 257
QY 241 GALLVRLQLQAL-----RVARMPLGLERSVRERFLP 269
DB 258 GLMLGLVNCFLVQKPKKPSCLQORDAKVHPV 290

RESULT 5
O88734 PRELIMINARY; PRT; 482 AA.
AC O88734;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE Similar to tumor necrosis factor receptor 2 Gene: Genomic Structure
DE P80 TNF-alpha receptor.
GN TNFR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98414512; PubMed=9740674;
RA Hurler B., Segade F., Rodriguez R., Ramos S.S., Lazo P.S.;
RT "The Mouse tumor Necrosis factor Receptor 2 Gene: Genomic Structure
  and Characterization of the two Transcripts.";
RL Genomics 52:79-98(1998).
DR EMBL; Y14619; CAA74969.1; -.
DR EMBL; Y14620; CAA74969.1; JOINED.
DR EMBL; Y14621; CAA74969.1; JOINED.

```

```

DR EMBL; Y14622; CAA74969.1; JOINED.
DR EMBL; Y14623; CAA74969.1; JOINED.
DR EMBL; Y14679; CAA74969.1; JOINED.
DR HSSP; Q92956; LJMA.
DR InterPro; IPR001368; TNFR_C6.
DR Pfam; PF00020; TNFR_C6; 4.
DR SMART; SM00208; TNFR_C6; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00500; TNFR_NGFR_2; 3.
KW Receptor.
SQ SEQUENCE 482 AA; 51106 MW; F6C15046B48FF83C CRC64;

Query Match 21.9%; Score 327; DB 11; Length 482;
Best Local Similarity 29.3%; Pred. No. 5.3e-21;
Matches 82; Conservative 43; Mismatches 109; Indels 46; Gaps 10;

QY 17 RVLCACCPGTFVQPCRRDPTTCGPPRHVYTFWNYLCRYCNVLCGR 69
DB 52 QMCCAKCPGQVKGFCNKTSDTVCADCEASMYTQVWNOFRITCLSCSSCSTD 111
QY 70 EEEARACHATHNRACRCRTGFF----AHAGF---CLEHASCPPGAGVIAPTG 122
DB 112 QVETRACCTKQNRKVCACEAGRYCALKTHSGSCRCQKRLSKCGFGVASSRAFN 171
QY 123 PEPGTFESASSSSSQCPHRCNTALGLALNVPGSSSHDTLCCT----SCTGF 178
DB 172 ACAPGTFSTTSSTVCRPHRICSIILA----IPGNASTDAVCAPESTLSAIP 227
QY 179 ABECERAVIDFAVAFQDISIKRLQRLQALEAPGEGMPTP-----RAGRAAL 233
DB 228 PPTTSQPLD-----QEPGSPQPSILTSI-----GSTPIEQSTKGGISL 277
QY 234 ELHGQDQDGLLVRLQLQAL-----RVARMPLGLERSVRERFLP 269
DB 278 SL-----GLMLGLVNCFLVQKPKKPSCLQORDAKVHPV 312

RESULT 6
O81VS6 PRELIMINARY; PRT; 457 AA.
AC O81VS6;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DE Similar to tumor necrosis factor receptor superfamily, member iB
DE (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC Strausberg R.;
RA Strausberg R.;
RL Submitted (JAN-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC042167; AAH42167.1; -.
KW Receptor.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 457 AA; 48120 MW; 1B634BBF1F5D77AC CRC64;

Query Match 21.3%; Score 317.5; DB 4; Length 457;
Best Local Similarity 30.3%; Pred. No. 3.5e-20;
Matches 80; Conservative 39; Mismatches 108; Indels 37; Gaps 9;

QY 25 PGTFVQPCRRDPTTCGPPRHVYTFWNYLCRYCNVLCGEREEERACHATHNRAC 84
DB 55 PQGHAKVPTKTSYDTCDCEDSTYTLQMNWPECLSCGSRCSDDQVETACTEQRNIC 114
QY 85 RCRTGTFFAHAG-----FCLHASCPPGAGVIAPTGSPQNTQCPPTFSASSSSE 138
DB 115 TCRPGWYCALSKQEGCRLCAPLKRCPGFGVAPRGTTSDVVKPCAPGTFSTSTDI 174
QY 139 CQPHRCNTALGLALNVPGSSSHDTLCCTCTGFPFLSTRVPGAECECERAVIDFA 198

```

```

Db 175 CRPHQCNVWA-----IPGNASMDAVCTSTS-----PTRSMAPGAVHLPQPV-----STRSQ 221
Qy 199 RLQRLLOALEAPE-----GWGPTPRA-----GRAALQLKLRLRLTELLGAQDCGALLVRLIQ 249
Db 222 H*QTPPESTAPSFLLPMPGSPPAEGSTGDFALPVGLVGYTAL-----GLLIIGVYN 276
Qy 250 AL---RVARMP-GLERSVREPLP 269
Db 277 CVIMTQVKKPLCLQREAKVHLP 300

RESULT 7
Q91ZM6 PRELIMINARY; PRT; 433 AA.
AC Q91ZM6;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor type II (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley;
RA Osburg B., Peiser C., Doemling D., Schomburg L., Voigt K., Bickel U.;
RT "TNF-receptors p60 and p80 are constitutively expressed by rat brain
RT capillary endothelial cells and participate in TNF-alpha transport
RT through the blood-brain barrier."
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF420214; AAL16021.1; -.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 3.
KW Receptor.
FT NON TER 1 433
FT NON TER 433
SQ SEQUENCE 433 AA; 45723 MW; 75736D835E72CA4A CRC64;

Query Match 21.0%; Score 313.5; DB 11; Length 433;
Best Local Similarity 35.1%; Pred. No. 7.6e-20;
Matches 59; Conservative 29; Mismatches 67; Indels 13; Gaps 4;

Qy 17 RLCAQCPPTGVQRCRDSPTTCGPPRHVYTOFWNYLRCRYCNVLCGEREEARAC 76
Db 32 QMCCAKCPGGQYAKHFCKNTSDTVCAACAGFTQVWHLHTCLSCSSCSDDDQVETENC 91
Qy 77 HATINRACRRTGFFA-----HAG-----FLEHASCPPGAGVIAPGTPSONTCQCPPTGTF 129
Db 92 TKKQNRVCACNADSYCALKLHSGNCRQCKMLSKCGFGFGVARSRTSNGNVICSAAPGTF 151
Qy 130 SASSSSSCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGTPPLSTRVP 177
Db 152 SDTTSSTVDVPHRICSLA-----IPGNASTDAVCASES---PTSGAVP 193

RESULT 8
Q98SM6 PRELIMINARY; PRT; 651 AA.
AC Q98SM6;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Death receptor 6.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=90311;

```

```

RN SEQUENCE FROM N.A.
RP Brigham J.T., Johnson A.L.;
RT "Expression of DR6 in the ovary."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF349908; AAK29666.2; -.
DR HSSP; PL9438; INCF.
DR InterPro; IPR00488; Death.
DR Pfam; PF00531; Death; 1.
DR Pfam; PF00020; TNFR_c6; 4.
DR SMART; SM00005; DEATH; 1.
DR SMART; SM00208; TNFR; 4.
DR PROSITE; PS00017; DEATH_DOMAIN; 1.
DR PROSITE; PS00652; TNFR_NGFR_1; 1.
DR PROSITE; PS00050; TNFR_NGFR_2; 1.
KW Receptor.
SQ SEQUENCE 651 AA; 71003 MW; BDC95A600DAB2C2A CRC64;

Query Match 19.2%; Score 287; DB 13; Length 651;
Best Local Similarity 33.5%; Pred. No. 2.7e-17;
Matches 54; Conservative 27; Mismatches 80; Indels 0; Gaps 0;

Qy 11 DAETGERLWCAQCPPTGVQRCRDSPTTCGPPRHVYTOFWNYLRCRYCNVLCGERE 70
Db 43 DRATQELICDKCPAGTVSKHCTKSTLRECSFCDGTFTKHENGIERCHPKCPCELP 102
Qy 71 EPARACHATHNRACRRTGFFAAGAGCFLHASCPPGAGVIAPGTPSONTCQCPPTGTF 130
Db 103 IEKTHCTALTDRCTCLSGTFOINDTCVYTCVPVGMGVKKGTEDEVRCCKPCLRGTF 162
Qy 131 ASSSSSSCCQPHRNCNTALGLALNVPGSSSHDTLCTCTGTP 171
Db 163 DVPSSVMKCKTYDCGKNMVYKFGTKESDNVCGSPASLP 203

RESULT 9
Q57108 PRELIMINARY; PRT; 348 AA.
AC Q57108;
DT 01-JUN-1998 (TREMBlrel. 06, Created)
DT 01-JUN-1998 (TREMBlrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
OS Xonkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-1970;
RA Loparev V.N., Parsons J.M., Beposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
RT orthopoxviruses to a particular species."
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U88142; AAB94367.1; -.
DR HSSP; Q92956; LJMA.
DR InterPro; IPR001368; TNFR_c6.
DR Pfam; PF00020; TNFR_c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR PROSITE; PS00050; TNFR_NGFR_2; 2.
KW Receptor.
SQ SEQUENCE 348 AA; 38212 MW; E555979057DEC91F CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred. No. 1.6e-16;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

Qy 10 RDAETGER-LVCAQCPPTGVQRCRDSPTTCGPPRHVYTOFWNYLRCRYCNVLCGE 68
Db 33 KDNEYRSNLCCSCPPGTVASRLCDKNTQCTPGSDTFTSHNNHLQACLSCNGRCD 92

```

```

RESULT 11
O57103 PRELIMINARY; PRT; 348 AA.
ID AC O57103;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Zaire-1979;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87847; AAB94364.1; -.
DR HSSP; Q92356; IJMA.
DR InterPro; IPR001368; TNFR.c6.
DR Pfam; PF0020; TNFR.c6; 2.
DR SMART; SM00208; TNFR; 2.
DR PROSITE; PS00652; TNFR_NGFR_1; 2.
DR DR POSITE; PS00652; TNFR_NGFR_2; 2.
DR Receptor.
SQ SEQUENCE 348 AA; 38184 MW; 34A5E668B27907B5 CRC64;

Query Match 18.4%; Score 275; DB 12; Length 348;
Best Local Similarity 33.1%; Pred.No.1.6e-18;
Matches 59; Conservative 29; Mismatches 82; Indels 8; Gaps 3;

Cy 10 RDAETGER-LVCAQCPPGTVEQRPCCRDSPTTCGCPCPRHYTQFWNYLERCRYCNVLCGE 68
Db 33 KDNEYSRNLCCLSCPGETYASRLCDSEKTNVTCQPCGSDFTTSHNHLOACLSCNGRCD 92
Cy 69 REBEARACHATHNRACNCRGTGFF-----AHAGFCLEHASCPGAGVIAPGTPSQNTQCQ 122
Db 93 NQVETRSCNTTHNRICEPCSPYVCLLKGSGCRTCISKTCGIGYGV-SGVTSGDVICS 151
Cy 123 PCPCGTFSSASSSEQOPHNCRTALGLANVPGSSSHDTILCTSCFFPLSTRVPGAE 180
Db 152 PCGPGTYSTVSSTKDCEPTSTNFYIDVINDLPVNDTSCRTTTTGLSESISTSE 209

RESULT 12
O57100 PRELIMINARY; PRT; 349 AA.
ID AC O57100;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Tumor necrosis factor receptor II homolog.
GN CRMB.
OS Monkeypox virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Orthopoxvirus.
OX NCBI_TaxID=10244;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Nigeria-1971;
RA Loparev V.N., Parsons J.M., Esposito J.J.;
RT "DNA sequence analysis as a criterion for allocation of the
orthopoxviruses to a particular species.";
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U87844; AAB94361.1; -.
DR HSSP; Q92356; IJMA.
DR InterPro; IPR001368; TNFR.c6.
DR Pfam; PF0020; TNFR.c6; 2.
DR SMART; SM00208; TNFR; 2.

```

[illegible]

